GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: September 5, 2004, 09:30:43 ; Search time 9.5 Seconds
(without alignments)
121.505 Million cell updates/sec

Title: US-09-730-174A-3
Perfect score: 59
Sequence: 1 SVSEIQLMHNLG 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 1581

Minimum DB seq length: 0
Maximum DB seq length: 12

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	21	35.6	12	2	S21205	Ig heavy chain V r
2	18	30.5	7	2	A58718	carnocin UI49 - Ca
3	18	30.5	9	2	S78420	ribosomal protein
4	18	30.5	10	2	A60589	sperm-activating p
5	18	30.5	10	2	B46453	e antigen p20e pre
6	17	28.8	7	2	I46868	alpha-myosin heavy
7	17	28.8	10	2	S28055	cytochrome b559 co
8	17	28.8	10	2	A37268	Ig heavy chain C r
9	16	27.1	9	2	S13636	coat protein beta
10	16	27.1	10	2	A47364	placental lactogen
11	15	25.4	7	2	S25266	pilE protein - Esc
12	15	25.4	7	2	S29735	polyphosphate-gluc
13	15	25.4	9	2	PW0002	chlorophyll a/b-bi
14	15	25.4	9	2	A56029	N-methylpurine DNA
15	15	25.4	10	2	S27873	hypothetical prote
16	15	25.4	11	2	A38841	rhodopsin homolog
17	15	25.4	11	2	S35490	type II site-speci
18	15	25.4	11	2	B41835	translation elonga
19	15	25.4	11	2	A40795	glycoprotein H-a -
20	15	25.4	12	2	A55837	5-aminoimidazole r
21	14	23.7	4	2	I38888	COI intron 16 prot
22	14	23.7	7	2	JN0859	peptidyl-dipeptida
23	14	23.7	7	2	T09512	NADH2 dehydrogenas
24	14	23.7	9	2	PT0238	Ig heavy chain CRD
25	14	23.7	10	1	SPPGNK	neuromedin K - pig
26	14	23.7	10	2	C61033	ranatachykinin C -
27	14	23.7	11	2	A55149	tetracenomycin A2
28	14	23.7	11	2	S60354	retinal oxidase -
29	14	23.7	11	2	B29806	acidic proline-ric
30	14	23.7	11	2	PH0904	T-cell receptor be
31	14	23.7	11	2	PH0924	T-cell receptor be
32	14	23.7	11	4	S41909	hypothetical prote
33	14	23.7	12	2	S25485	transcription fact
34	14	23.7	12	2	G49410	t-complex polypept
35	14	23.7	12	2	S71034	potB protein - Sal
36	14	23.7	12	2	C60529	hemocyanin 1 - gre
37	14	23.7	12	2	PH1190	T-cell receptor al
38	14	23.7	12	2	PH1187	T-cell receptor al
39	14	23.7	12	2	PH1189	T-cell receptor al
40	14	23.7	12	2	I41235	glutamine-tRNA lig
41	13	22.0	6	2	A20186	fatty-acid synthas
42	13	22.0	8	2	T14906	hypothetical prote
43	13	22.0	8	2	JS0316	leucokinin VI - Ma
44	13	22.0	8	2	PH1618	Ig H chain V-D-J r
45	13	22.0	9	2	JN0026	sperm-activating p

ALIGNMENTS

RESULT 1
S21205
Ig heavy chain V region - human
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 16-Aug-1996
C;Accession: S21205
R;Makiya, R.; Stigbrand, T.
Eur. J. Biochem. 205, 341-345, 1992
A;Title: Placental alkaline phosphatase has a binding site for the human immunoglobulin-
A;Reference number: S21205; MUID:92209522; PMID:1555592
A;Accession: S21205
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-12 <MAK>
C;Keywords: heterotetramer; immunoglobulin

Query Match 35.6%; Score 21; DB 2; Length 12;
Best Local Similarity 44.4%; Pred. No. 6.5e+02;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

```
Qy          4 EIQLMHNLG 12
              |:||: : |
Db          1 EVQLVESGG 9
```

RESULT 2
A58718
carnocin UI49 - Carnobacterium sp. (fragment)
C;Species: Carnobacterium sp.
C;Date: 23-Jan-1998 #sequence_revision 30-Jan-1998 #text_change 30-Jan-1998
C;Accession: A58718
R;Stoffels, G.; Nissen-Meyer, J.; Gudmundsdottir, A.; Sletten, K.; Holo, H.; Nes, I.F.
Appl. Environ. Microbiol. 58, 1417-1422, 1992
A;Title: Purification and characterization of a new bacteriocin isolated from a Carnoba
A;Reference number: A58718; MUID:92321768; PMID:1622206
A;Accession: A58718
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-7 <STO>
C;Keywords: antibiotic; lanthionine

Query Match 30.5%; Score 18; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          3 SEIQ 6
              ||||
Db          2 SEIQ 5
```

RESULT 3
S78420

```
ribosomal protein RL41, mitochondrial [validated] - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 25-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 21-Jul-2000
C;Accession: S78420
R;Goldschmidt-Reisin, S.; Graack, H.R.
submitted to the Protein Sequence Database, February 1998
A;Reference number: S78411
A;Accession: S78420
A;Molecule type: protein
A;Residues: 1-9 <GOL>
A;Note: the protein is designated as mitochondrial ribosomal protein L41
C;Keywords: mitochondrion; protein biosynthesis; ribosome

  Query Match             30.5%;  Score 18;  DB 2;  Length 9;
  Best Local Similarity   75.0%;  Pred. No. 2.8e+05;
  Matches    3;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          9 HNLG 12
              | ||
Db          5 HRLG 8


RESULT 4
A60589
sperm-activating peptide (Tyr-2, Asn-3, Gly-5, Ile-9, Asp-10 SAP-I) - slate-pencil urchi
C;Species: Heterocentrotus mamillatus
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 18-Aug-2000
C;Accession: A60589
R;Yoshino, K.I.; Kajiura, H.; Nomura, K.; Takao, T.; Shimonishi, Y.; Kurita, M.; Yamaguc
Comp. Biochem. Physiol. B 94, 739-751, 1989
A;Title: A halogenated amino acid-containing sperm activating peptide and its related pe
otus nudus, Echinometra mathaei and Heterocentrotus mammillatus.
A;Reference number: A60527
A;Accession: A60589
A;Molecule type: protein
A;Residues: 1-10 <YOS>
C;Superfamily: unassigned animal peptides

  Query Match             30.5%;  Score 18;  DB 2;  Length 10;
  Best Local Similarity   75.0%;  Pred. No. 2e+03;
  Matches    3;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          9 HNLG 12
              :|||
Db          2 YNLG 5


RESULT 5
B46453
e antigen p20e precursor - hepatitis B virus (subtype adr) (fragment)
N;Alternate names: HBe antigen precursor
N;Contains: e antigen
C;Species: hepatitis B virus, HBV
A;Variety: subtype adr
C;Date: 18-Jun-1993 #sequence_revision 08-Nov-1996 #text_change 15-Aug-1997
C;Accession: B46453
R;Takahashi, K.; Kishimoto, S.; Ohori, K.; Yoshizawa, H.; Machida, A.; Ohnuma, H.; Tsuda
J. Immunol. 147, 3156-3160, 1991
A;Title: Molecular heterogeneity of e antigen polypeptides in sera from carriers of hepa
A;Reference number: A46453; MUID:92013147; PMID:1717588
A;Accession: B46453
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-10 <TAK>
A;Experimental source: subtype adr
A;Note: sequence extracted from NCBI backbone (NCBIP:60243)
F;1-10/Domain: signal sequence (fragment) #status predicted <SIG>

  Query Match             30.5%;  Score 18;  DB 2;  Length 10;
  Best Local Similarity   60.0%;  Pred. No. 2e+03;
  Matches    3;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          5 IQLMH 9
                :|| |
Db          1 MQLFH 5


RESULT 6
I46868
alpha-myosin heavy chain - rabbit (fragment)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 14-Feb-1997 #sequence_revision 14-Feb-1997 #text_change 05-Nov-1999
C;Accession: I46868
R;Friedman, D.J.; Umeda, P.K.; Sinha, A.M.; Hsu, H.
Proc. Natl. Acad. Sci. U.S.A. 81, 3044-3048, 1984
A;Title: Characterization of genomic clones specifying rabbit alpha- and beta-ventricula
A;Reference number: I46868; MUID:84221901; PMID:6328491
A;Accession: I46868
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-7 <FRI>
A;Cross-references: GB:K01698; NID:g165538; PIDN:AAA31415.1; PID:g165539

  Query Match             28.8%;  Score 17;  DB 2;  Length 7;
  Best Local Similarity   60.0%;  Pred. No. 2.8e+05;
  Matches    3;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          6 QLMHN 10
              | ||:
Db          1 QKMHD 5


RESULT 7
S28055
cytochrome b559 component psbF - pepper chloroplast (fragment)
C;Species: chloroplast Capsicum annuum (pepper)
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 11-Jun-1999
C;Accession: S28055
R;Kuntz, M.; Camara, B.; Weil, J.H.; Schantz, R.
Plant Mol. Biol. 20, 1185-1188, 1992
A;Title: The psbL gene from bell pepper (Capsicum annuum): plastid RNA editing also occu
A;Reference number: S28055; MUID:93099270; PMID:1463853
A;Accession: S28055
A;Molecule type: DNA
A;Residues: 1-10 <KUN>
A;Cross-references: EMBL:X65570; NID:g14344; PIDN:CAA46539.1; PID:g415734
C;Genetics:
A;Gene: psbF
A;Genome: chloroplast
C;Superfamily: cytochrome b559 component F
C;Keywords: chloroplast; photosynthesis; photosystem II; thylakoid

  Query Match             28.8%;  Score 17;  DB 2;  Length 10;
  Best Local Similarity   37.5%;  Pred. No. 3.1e+03;
  Matches    3;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 SVSEIQLM 8
              |:| :| :
Db          1 SISAMQFI 8


RESULT 8
A37268
Ig heavy chain C region (129) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 19-Mar-1997 #sequence_revision 13-Mar-1998 #text_change 13-Mar-1998
C;Accession: A37268
R;Ruff-Jamison, S.; Campos-Gonzalez, R.; Glenney Jr., J.R.
J. Biol. Chem. 266, 6607-6613, 1991
A;Title: Heavy and light chain variable region sequences and antibody properties of anti
A;Reference number: A38740; MUID:91177923; PMID:1706720
A;Accession: A37268
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-10 <RUF>
```

```
  Query Match             28.8%;  Score 17;  DB 2;  Length 10;
  Best Local Similarity   44.4%;  Pred. No. 3.1e+03;
  Matches    4;  Conservative    1;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          4 EIQLMHNLG 12
              | |   |:|
Db          1 ESQSFPNVG 9


RESULT 9
S13636
coat protein beta chain, Golgi-derived - rabbit (fragment)
N;Alternate names: beta-COP protein
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 19-Mar-1997 #sequence_revision 24-Mar-1999 #text_change 24-Mar-1999
C;Accession: S13636
R;Serafini, T.; Stenbeck, G.; Brecht, A.; Lottspeich, F.; Orci, L.; Rothman, J.E.; Wiela
Nature 349, 215-220, 1991
A;Title: A coat subunit of Golgi-derived non-clathrin-coated vesicles with homology to t
A;Reference number: S13636; MUID:91101693; PMID:1898984
A;Accession: S13636
A;Molecule type: protein
A;Residues: 1-9 <SER>
C;Superfamily: coatomer complex beta chain
C;Keywords: Golgi apparatus; protein transport

  Query Match             27.1%;  Score 16;  DB 2;  Length 9;
  Best Local Similarity   37.5%;  Pred. No. 2.8e+05;
  Matches    3;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 SVSEIQLM 8
              |: ||  ::
Db          1 SLGEIPIV 8


RESULT 10
A47364
placental lactogen-I precursor - mouse (fragment)
C;Species: Mus sp. (mouse)
C;Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 12-Aug-1996
C;Accession: A47364
R;Shida, M.M.; Ng, Y.K.; Soares, M.J.; Linzer, D.I.
Mol. Endocrinol. 7, 181-188, 1993
A;Title: Trophoblast-specific transcription from the mouse placental lactogen-I gene prc
A;Reference number: A47364; MUID:93225959; PMID:8469232
A;Accession: A47364
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-10 <RES>
A;Cross-references: GB:S58124; NID:g299449

  Query Match             27.1%;  Score 16;  DB 2;  Length 10;
  Best Local Similarity   57.1%;  Pred. No. 4.9e+03;
  Matches    4;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          5 IQLMHNL 11
              :|| ||
Db          1 MQLTLNL 7


RESULT 11
S25266
pilE protein - Escherichia coli (fragment)
C;Species: Escherichia coli
C;Date: 28-May-1993 #sequence_revision 28-May-1993 #text_change 11-Jun-1993
C;Accession: S25266
R;Dupuy, B.; Taha, M.K.; Possot, O.; Marchal, C.; Pugsley, A.P.
Mol. Microbiol. 6, 1887-1894, 1992
A;Title: PulO, a component of the pullulanase secretion pathway of Klebsiella oxytoca, c
A;Reference number: S25266; MUID:92374839; PMID:1354833
A;Accession: S25266
A;Molecule type: protein
A;Residues: 1-7 <DUP>
C;Genetics:
A;Gene: pilE

  Query Match             25.4%;  Score 15;  DB 2;  Length 7;
  Best Local Similarity   75.0%;  Pred. No. 2.8e+05;
  Matches    3;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 IQLM 8
              |:||
Db          4 IELM 7


RESULT 12
S29735
polyphosphate-glucose phosphotransferase (EC 2.7.1.63) - Propionibacterium freudenreichi
C;Species: Propionibacterium freudenreichii subsp. shermanii
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 03-Jun-2002
C;Accession: S29735
R;Phillips, N.F.B.; Horn, P.J.; Wood, H.G.
Arch. Biochem. Biophys. 300, 309-319, 1993
A;Title: The polyphosphate- and ATP-dependent glucokinase from Propionibacterium shermar
A;Reference number: S29735; MUID:93143332; PMID:8380966
A;Accession: S29735
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-7 <PHI>
C;Keywords: phosphotransferase

  Query Match             25.4%;  Score 15;  DB 2;  Length 7;
  Best Local Similarity   75.0%;  Pred. No. 2.8e+05;
  Matches    3;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          9 HNLG 12
              | ||
Db          2 HVLG 5


RESULT 13
PW0002
chlorophyll a/b-binding protein 31K - green alga (Dunaliella tertiolecta) (fragment)
N;Alternate names: photosystem II light-harvesting chlorophyll 31K protein
C;Species: Dunaliella tertiolecta
C;Date: 24-Nov-1999 #sequence_revision 24-Nov-1999 #text_change 24-Nov-1999
C;Accession: PW0002
R;LaRoche, J.; Bennett, J.; Falkowski, P.G.
Gene 95, 165-171, 1990
A;Title: Characterization of a cDNA encoding for the 28.5-kDa LHCII apoprotein from the
A;Reference number: JW0040; MUID:91065528; PMID:2249775
A;Accession: PW0002
A;Molecule type: protein
A;Residues: 1-9 <LAR>
C;Superfamily: chlorophyll a/b-binding protein
C;Keywords: chloroplast; grana; light-harvesting complex; membrane adhesion; membrane p

  Query Match             25.4%;  Score 15;  DB 2;  Length 9;
  Best Local Similarity   60.0%;  Pred. No. 2.8e+05;
  Matches    3;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 EIQLM 8
              |:| |
Db          5 EMQAM 9


RESULT 14
A56029
N-methylpurine DNA glycosylase - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 19-Jan-1996 #sequence_revision 19-Jan-1996 #text_change 19-Jan-1996
C;Accession: A56029
R;Roy, R.; Brooks, C.; Mitra, S.
Biochemistry 33, 15131-15140, 1994
A;Title: Purification and biochemical characterization of recombinant N-methylpurine-DN
A;Reference number: A56029; MUID:95092772; PMID:7999773
```

A;Accession: A56029
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-9 <ROY>

Query Match 25.4%; Score 15; DB 2; Length 9;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 9 HNLG 12
| :|
Db 3 HEVG 6

RESULT 15
S27873
hypothetical protein 2 LRH-1 5'-region - mouse
C;Species: Mus musculus (house mouse)
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 18-Aug-2000
C;Accession: S27873
R;Tugwood, J.D.; Issemann, I.; Green, S.
submitted to the EMBL Data Library, February 1992
A;Description: LRH-1: A nuclear hormone receptor active in the absence of exogenous liga
A;Reference number: S27873
A;Accession: S27873
A;Molecule type: mRNA
A;Residues: 1-10 <TUG>
A;Cross-references: EMBL:M81385; NID:g198872; PIDN:AAA39446.1; PID:g198874
C;Superfamily: unassigned leader peptides

Query Match 25.4%; Score 15; DB 2; Length 10;
Best Local Similarity 50.0%; Pred. No. 7.6e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SVSEIQ 6
::| ||
Db 5 NLSHIQ 10

Search completed: September 5, 2004, 09:37:43
Job time : 10.5 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: September 5, 2004, 09:27:07 ; Search time 6.5 Seconds
(without alignments)
96.130 Million cell updates/sec

Title: US-09-730-174A-3
Perfect score: 59
Sequence: 1 SVSEIQLMHNLG 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 501

Minimum DB seq length: 0
Maximum DB seq length: 12

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	18	30.5	7	1	LANC_CARUI	P36960 carnobacter
2	17	28.8	10	1	PSBF_CAPAN	Q03367 capsicum an
3	16	27.1	8	1	ALL6_CYDPO	P82157 cydia pomon
4	16	27.1	8	1	FUSS_FUSSO	P81010 fusarium so
5	16	27.1	10	1	RRPL_PHODV	P35946 phocine dis
6	16	27.1	11	1	EFG_CLOPA	P81350 clostridium
7	15	25.4	11	1	PVK1_PERAM	P41837 periplaneta
8	15	25.4	11	1	T2P1_PROVU	P31031 proteus vul
9	14	23.7	6	1	TRPI_PSEPU	P36414 pseudomonas
10	14	23.7	7	1	ALL7_CYDPO	P82158 cydia pomon
11	14	23.7	8	1	AL18_CARMA	P81821 carcinus ma
12	14	23.7	8	1	ALL1_CYDPO	P82152 cydia pomon
13	14	23.7	9	1	FAR8_MACRS	P83281 macrobrachi
14	14	23.7	9	1	UF02_MOUSE	P38640 mus musculu
15	14	23.7	10	1	AL19_CARMA	P81822 carcinus ma
16	14	23.7	10	1	TEMK_RANTE	P56923 rana tempor
17	14	23.7	10	1	TKNC_RANCA	P22690 rana catesb
18	14	23.7	10	1	TKNK_PIG	P01292 sus scrofa
19	14	23.7	11	1	ASL1_BACSE	P83146 bacteroides
20	14	23.7	12	1	CD11_LITXA	P56245 litoria xan
21	14	23.7	12	1	CD14_LITXA	P56246 litoria xan
22	14	23.7	12	1	HCY1_CARMA	P83176 carcinus ma
23	14	23.7	12	1	PORD_METTM	P80903 methanobact
24	14	23.7	12	1	RS19_TOBBP	Q56251 tomato big
25	13	22.0	8	1	LCK4_LEUMA	P21143 leucophaea
26	13	22.0	8	1	LCK6_LEUMA	P19988 leucophaea
27	13	22.0	9	1	MOSH_CLYJA	P19852 clypeaster
28	13	22.0	9	1	PPK1_PERAM	P82691 periplaneta
29	13	22.0	11	1	CSI5_BACSU	P81095 bacillus su
30	13	22.0	11	1	Q2OA_COMTE	P80464 comamonas t
31	13	22.0	12	1	PA2B_VIPBO	P31859 vipera beru
32	13	22.0	12	1	PPK4_PERFU	P82690 periplaneta
33	13	22.0	12	1	UR2_POLSP	P81022 polyodon sp
34	12	20.3	9	1	FIBB_PAPHA	P19343 papio hamad
35	12	20.3	9	1	RE42_LITRU	P82075 litoria rub
36	12	20.3	10	1	GLEM_HUMAN	P02728 homo sapien
37	12	20.3	10	1	GON1_CLUPA	P81749 clupea pall
38	12	20.3	10	1	GON2_CHEPR	P80678 chelyosoma
39	12	20.3	10	1	HTF1_ROMMI	P18110 romalea mic
40	12	20.3	10	1	HTF_HELZE	P16353 heliothis z
41	12	20.3	10	1	SYK_CAMUP	Q46464 campylobact
42	12	20.3	10	1	TKNB_RANRI	P29135 rana ridibu
43	12	20.3	11	1	CXL1_CONMR	P58807 conus marmo
44	12	20.3	11	1	HS70_PINPS	P81672 pinus pinas
45	12	20.3	12	1	HEP1_BACSE	P83054 bacteroides

ALIGNMENTS

RESULT 1
LANC_CARUI
ID LANC_CARUI STANDARD; PRT; 7 AA.
AC P36960;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Lantibiotic carnocin UI49 (Fragment).
OS Carnobacterium sp. (strain UI49).
OC Bacteria; Firmicutes; Lactobacillales; Carnobacteriaceae;
OC Carnobacterium.
OX NCBI_TaxID=35782;
RN [1]
RP SEQUENCE.
RX MEDLINE=92321768; PubMed=1622206;
RA Stoffels G., Nissen-Meyer J., Gudmundsdottir A., Sletten K., Holo H.,
RA Nes I.F.;
RT "Purification and characterization of a new bacteriocin isolated from
RT a Carnobacterium sp.";
RL Appl. Environ. Microbiol. 58:1417-1422(1992).
CC -!- FUNCTION: Lanthionine-containing peptide antibiotic (lantibiotic).
CC Active on Gram-positive bacteria.
KW Antibiotic; Bacteriocin; Lantibiotic.
FT NON_TER 7 7
SQ SEQUENCE 7 AA; 786 MW; 741776D05B05B810 CRC64;

Query Match 30.5%; Score 18; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          3 SEIQ 6
              ||||
Db          2 SEIQ 5
```

RESULT 2
PSBF_CAPAN
ID PSBF_CAPAN STANDARD; PRT; 10 AA.
AC Q03367;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Cytochrome b559 beta subunit (PSII reaction center subunit VI)
DE (Fragment).
GN PSBF.
OS Capsicum annuum (Bell pepper).
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC lamiids; Solanales; Solanaceae; Capsicum.
OX NCBI_TaxID=4072;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Lamuyo; TISSUE=Fruit, and Leaf;
RX MEDLINE=93099270; PubMed=1463853;
RA Kuntz M., Camara B., Weil J.-H., Schantz R.;

```
RT   "The psbL gene from bell pepper (Capsicum annuum): plastid RNA
RT   editing also occurs in non-photosynthetic chromoplasts.";
RL   Plant Mol. Biol. 20:1185-1188(1992).
CC   -!- FUNCTION: This b-type cytochrome is tightly associated with the
CC       reaction center of photosystem II and possibly is part of the
CC       water-oxidation complex.
CC   -!- SUBUNIT: Heterodimer of an alpha subunit and a beta subunit.
CC   -!- SIMILARITY: Belongs to the psbE / psbF family.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X65570; CAA46539.1; -.
DR   PIR; S28055; S28055.
DR   HAMAP; MF_00643; -; 1.
DR   InterPro; IPR006216; Cyt_b559.
DR   PROSITE; PS00537; CYTOCHROME_B559; PARTIAL.
KW   Chloroplast; Photosystem II; Heme; Electron transport; Transmembrane.
FT   NON_TER       1      1
FT   TRANSMEM      <1      5       BY SIMILARITY.
FT   DOMAIN         6     10       LUMENAL (POTENTIAL).
SQ   SEQUENCE   10 AA;  1180 MW;  817D0F59D6D69DC5 CRC64;

  Query Match             28.8%;  Score 17;  DB 1;  Length 10;
  Best Local Similarity   37.5%;  Pred. No. 1.9e+03;
  Matches    3;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 SVSEIQLM 8
              |:|  :| :
Db          1 SISAMQFI 8


RESULT 3
ALL6_CYDPO
ID   ALL6_CYDPO     STANDARD;      PRT;     8 AA.
AC   P82157;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   Cydiastatin 6.
OS   Cydia pomonella (Codling moth).
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC   Tortricoidea; Tortricidae; Olethreutinae; Cydia.
OX   NCBI_TaxID=82600;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Larva;
RX   MEDLINE=98054539; PubMed=9392829;
RA   Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Winstanley D.,
RA   Davey M., East P.D., Thorpe A.;
RT   "Lepidopteran peptides of the allatostatin superfamily.";
RL   Peptides 18:1301-1309(1997).
CC   -!- SIMILARITY: Belongs to the allatostatin family.
KW   Neuropeptide; Amidation.
FT   MOD_RES       8      8       AMIDATION.
SQ   SEQUENCE   8 AA;  936 MW;  0B2879C45B573767 CRC64;

  Query Match             27.1%;  Score 16;  DB 1;  Length 8;
  Best Local Similarity   40.0%;  Pred. No. 1.4e+05;
  Matches    2;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          8 MHNLG 12
              ::| |
Db          3 LYNFG 7


RESULT 4
FUSS_FUSSO
ID   FUSS_FUSSO     STANDARD;      PRT;     8 AA.
AC   P81010;
DT   15-JUL-1998 (Rel. 36, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Allergen Fus s I3596* (Fragment).
OS   Fusarium solani (subsp. pisi) (Nectria haematococca).
OC   Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC   Hypocreomycetidae; Hypocreales; Nectriaceae; Nectria.
OX   NCBI_TaxID=70791;
RN   [1]
RP   SEQUENCE.
RC   STRAIN=IARI 3596; TISSUE=Mycelium;
RA   Verma J., Gangal S.V.;
RL   Submitted (JUL-1997) to Swiss-Prot.
CC   -!- ALLERGEN: Causes an allergic reaction in human.
KW   Allergen.
FT   NON_TER       8      8
SQ   SEQUENCE   8 AA;  898 MW;  C372C441F5B69041 CRC64;

  Query Match             27.1%;  Score 16;  DB 1;  Length 8;
  Best Local Similarity   40.0%;  Pred. No. 1.4e+05;
  Matches    2;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 LMHNL 11
              : |::
Db          3 MSHNV 7


RESULT 5
RRPL_PHODV
ID   RRPL_PHODV     STANDARD;      PRT;    10 AA.
AC   P35946;
DT   01-JUN-1994 (Rel. 29, Created)
DT   01-JUN-1994 (Rel. 29, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   RNA polymerase beta subunit (EC 2.7.7.48) (Large structural protein)
DE   (L protein) (Fragment).
GN   L.
OS   Phocine distemper virus (PDV).
OC   Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC   Paramyxoviridae; Paramyxovirinae; Morbillivirus.
OX   NCBI_TaxID=11240;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Ulster/88;
RX   MEDLINE=92268877; PubMed=1588321;
RA   Curran M.D., O'Loan D., Kennedy S., Rima B.K.;
RT   "Molecular characterization of phocine distemper virus: gene order
RT   and sequence of the gene encoding the attachment (H) protein.";
RL   J. Gen. Virol. 73:1189-1194(1992).
CC   -!- FUNCTION: Probable component of the active polymerase. It may
CC       function in mRNA synthesis, capping, methylation and poly(A)
CC       synthesis of newly synthesized viral mRNAs, RNA editing of the P
CC       gene transcript, and protein kinase activity.
CC   -!- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
CC       {RNA}(N).
CC   -!- SIMILARITY: Belongs to the paramyxoviruses L protein family.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; D10371; BAA01208.1; -.
KW   Transferase; RNA-directed RNA polymerase.
FT   NON_TER      10     10
SQ   SEQUENCE   10 AA;  1105 MW;  9C2B7FD452D5A2D5 CRC64;
```

```
  Query Match             27.1%;  Score 16;  DB 1;  Length 10;
  Best Local Similarity   50.0%;  Pred. No. 3e+03;
  Matches    4;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 SVSEIQLM 8
              |||  |::
Db          3 SVSVNQIL 10


RESULT 6
EFG_CLOPA
ID   EFG_CLOPA      STANDARD;      PRT;    11 AA.
AC   P81350;
DT   15-JUL-1998 (Rel. 36, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Elongation factor G (EF-G) (CP 5) (Fragment).
GN   FUSA.
OS   Clostridium pasteurianum.
OC   Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC   Clostridium.
OX   NCBI_TaxID=1501;
RN   [1]
RP   SEQUENCE.
RC   STRAIN=W5;
RX   MEDLINE=98291870; PubMed=9629918;
RA   Flengsrud R., Skjeldal L.;
RT   "Two-dimensional gel electrophoresis separation and N-terminal
RT   sequence analysis of proteins from Clostridium pasteurianum W5.";
RL   Electrophoresis 19:802-806(1998).
CC   -!- FUNCTION: This protein promotes the GTP-dependent translocation of
CC       the nascent protein chain from the A-site to the P-site of the
CC       ribosome.
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC   -!- SIMILARITY: Belongs to the GTP-binding elongation factor family.
CC       EF-G/EF-2 subfamily.
DR   InterPro; IPR000795; EF_GTPbind.
DR   PROSITE; PS00301; EFACTOR_GTP; PARTIAL.
KW   Elongation factor; Protein biosynthesis; GTP-binding.
FT   NON_TER      11     11
SQ   SEQUENCE   11 AA;  1337 MW;  412E71F1D9C33B17 CRC64;

  Query Match             27.1%;  Score 16;  DB 1;  Length 11;
  Best Local Similarity   25.0%;  Pred. No. 3.3e+03;
  Matches    2;  Conservative    3;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          5 IQLMHNLG 12
              ::   |:|
Db          4 LEKFQNIG 11


RESULT 7
PVK1_PERAM
ID   PVK1_PERAM     STANDARD;      PRT;    11 AA.
AC   P41837;
DT   01-NOV-1995 (Rel. 32, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Periviscerokinin-1 (Pea-PVK-1).
OS   Periplaneta americana (American cockroach).
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattoidea;
OC   Blattidae; Periplaneta.
OX   NCBI_TaxID=6978;
RN   [1]
RP   SEQUENCE, AND SYNTHESIS.
RC   TISSUE=Abdominal perisympathetic organs;
RX   MEDLINE=95232021; PubMed=7716075;
RA   Predel R., Linde D., Rapus J., Vettermann S., Penzlin H.;
RT   "Periviscerokinin (Pea-PVK): a novel myotropic neuropeptide from the
RT   perisympathetic organs of the American cockroach.";
RL   Peptides 16:61-66(1995).
CC   -!- FUNCTION: MYOACTIVE PEPTIDE; HAS EXCITORY ACTIONS ON THE
CC       HYPERNEURAL MUSCLE.
KW   Neuropeptide; Amidation.
FT   MOD_RES      11     11       AMIDATION.
SQ   SEQUENCE   11 AA;  1114 MW;  39DB5419D7605728 CRC64;

  Query Match             25.4%;  Score 15;  DB 1;  Length 11;
  Best Local Similarity   50.0%;  Pred. No. 5.1e+03;
  Matches    3;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          5 IQLMHN 10
              | :| |
Db          6 IPVMRN 11


RESULT 8
T2P1_PROVU
ID   T2P1_PROVU     STANDARD;      PRT;    11 AA.
AC   P31031;
DT   01-JUL-1993 (Rel. 26, Created)
DT   01-JUL-1993 (Rel. 26, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Type II restriction enzyme PvuI (EC 3.1.21.4) (Endonuclease PvuI)
DE   (R.PvuI) (Fragment).
GN   PVUIR.
OS   Proteus vulgaris.
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC   Enterobacteriaceae; Proteus.
OX   NCBI_TaxID=585;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=ATCC 13315;
RX   MEDLINE=93087186; PubMed=1454536;
RA   Smith M.D., Longo M., Gerard G.F., Chatterjee D.K.;
RT   "Cloning and characterization of genes for the PvuI restriction and
RT   modification system.";
RL   Nucleic Acids Res. 20:5743-5747(1992).
CC   -!- FUNCTION: RECOGNIZES THE DOUBLE-STRANDED SEQUENCE CGATCG AND
CC       CLEAVES AFTER T-4.
CC   -!- CATALYTIC ACTIVITY: Endonucleolytic cleavage of DNA to give
CC       specific double-stranded fragments with terminal 5'-phosphates.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; L04163; AAA25660.1; -.
DR   PIR; S35490; S35490.
DR   REBASE; 1541; PvuI.
KW   Restriction system; Hydrolase; Nuclease; Endonuclease.
FT   NON_TER       1      1
SQ   SEQUENCE   11 AA;  1300 MW;  9F0CDE7955B72B1A CRC64;

  Query Match             25.4%;  Score 15;  DB 1;  Length 11;
  Best Local Similarity   60.0%;  Pred. No. 5.1e+03;
  Matches    3;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 SVSEI 5
              || |:
Db          2 SVDEL 6


RESULT 9
TRPI_PSEPU
ID   TRPI_PSEPU     STANDARD;      PRT;     6 AA.
AC   P36414;
DT   01-JUN-1994 (Rel. 29, Created)
DT   01-JUN-1994 (Rel. 29, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   HTH-type transcriptional regulator trpI (TrpBA operon transcriptional
```

```
DE   activator) (Fragment).
GN   TRPI.
OS   Pseudomonas putida.
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC   Pseudomonadaceae; Pseudomonas.
OX   NCBI_TaxID=303;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=PPG1 C1S;
RX   MEDLINE=89335826; PubMed=2503057;
RA   Eberly L., Crawford I.P.;
RT   "DNA sequence of the tryptophan synthase genes of Pseudomonas
RT   putida.";
RL   Biochimie 71:521-531(1989).
CC   -!- FUNCTION: ACTIVATES THE EXPRESSION OF THE TRPBA GENES ENCODING
CC       THE TWO TRYPTOPHAN SYNTHASE SUBUNITS. IN THE ABSENCE OF THE
CC       INDUCER (INDOLEGLYCEROL PHOSPHATE), TRPI BINDS UPSTREAM OF THE
CC       TRPAB OPERON, OVERLAPPING ITS OWN PROMOTER REGION.
CC   -!- SIMILARITY: Contains 1 HTH lysR-type DNA-binding domain.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; X13299; CAA31660.1; -.
DR   InterPro; IPR000847; HTH_LysR.
DR   PROSITE; PS50931; HTH_LYSR; PARTIAL.
KW   Tryptophan biosynthesis; Transcription regulation; Activator;
KW   DNA-binding.
FT   NON_TER       6       6
SQ   SEQUENCE   6 AA;  683 MW;  77672AA1EDD6F000 CRC64;

  Query Match             23.7%;  Score 14;  DB 1;  Length 6;
  Best Local Similarity   40.0%;  Pred. No. 1.4e+05;
  Matches    2;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 LMHNL 11
              : |:|
Db          1 MAHDL 5


RESULT 10
ALL7_CYDPO
ID   ALL7_CYDPO     STANDARD;      PRT;     7 AA.
AC   P82158;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   Cydiastatin 7.
OS   Cydia pomonella (Codling moth).
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC   Tortricoidea; Tortricidae; Olethreutinae; Cydia.
OX   NCBI_TaxID=82600;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Larva;
RX   MEDLINE=98054539; PubMed=9392829;
RA   Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Winstanley D.,
RA   Davey M., East P.D., Thorpe A.;
RT   "Lepidopteran peptides of the allatostatin superfamily.";
RL   Peptides 18:1301-1309(1997).
CC   -!- SIMILARITY: Belongs to the allatostatin family.
KW   Neuropeptide; Amidation.
FT   MOD_RES       7       7       AMIDATION.
SQ   SEQUENCE   7 AA;  873 MW;  672879CABB569350 CRC64;

  Query Match             23.7%;  Score 14;  DB 1;  Length 7;
  Best Local Similarity   40.0%;  Pred. No. 1.4e+05;
  Matches    2;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          8 MHNLG 12
              |:: |
Db          2 MYDFG 6


RESULT 11
AL18_CARMA
ID   AL18_CARMA     STANDARD;      PRT;     8 AA.
AC   P81821;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   Carcinustatin 18.
OS   Carcinus maenas (Common shore crab) (Green crab).
OC   Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC   Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC   Eubrachyura; Portunoidea; Portunidae; Carcinus.
OX   NCBI_TaxID=6759;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Cerebral ganglion, and Thoracic ganglion;
RX   MEDLINE=98121193; PubMed=9461295;
RA   Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
RA   Thorpe A.;
RT   "Isolation and identification of multiple neuropeptides of the
RT   allatostatin superfamily in the shore crab Carcinus maenas.";
RL   Eur. J. Biochem. 250:727-734(1997).
CC   -!- FUNCTION: May act as a neurotransmitter or neuromodulator.
CC   -!- SIMILARITY: Belongs to the allatostatin family.
KW   Neuropeptide; Amidation; Multigene family.
FT   MOD_RES       8       8       AMIDATION (POTENTIAL).
SQ   SEQUENCE   8 AA;  919 MW;  C82879D5AB569AB5 CRC64;

  Query Match             23.7%;  Score 14;  DB 1;  Length 8;
  Best Local Similarity   40.0%;  Pred. No. 1.4e+05;
  Matches    2;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          8 MHNLG 12
              |:: |
Db          3 MYSFG 7


RESULT 12
ALL1_CYDPO
ID   ALL1_CYDPO     STANDARD;      PRT;     8 AA.
AC   P82152;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   Cydiastatin 1.
OS   Cydia pomonella (Codling moth).
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC   Tortricoidea; Tortricidae; Olethreutinae; Cydia.
OX   NCBI_TaxID=82600;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Larva;
RX   MEDLINE=98054539; PubMed=9392829;
RA   Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Winstanley D.,
RA   Davey M., East P.D., Thorpe A.;
RT   "Lepidopteran peptides of the allatostatin superfamily.";
RL   Peptides 18:1301-1309(1997).
CC   -!- SIMILARITY: Belongs to the allatostatin family.
KW   Neuropeptide; Amidation.
FT   MOD_RES       8       8       AMIDATION.
SQ   SEQUENCE   8 AA;  934 MW;  C82879C45B51F775 CRC64;

  Query Match             23.7%;  Score 14;  DB 1;  Length 8;
  Best Local Similarity   50.0%;  Pred. No. 1.4e+05;
  Matches    2;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;
```

```
Qy          9 HNLG 12
              :| |
Db          4 YNFG 7
```

```
RESULT 13
FAR8_MACRS
ID   FAR8_MACRS     STANDARD;      PRT;     9 AA.
AC   P83281;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   FMRFamide-like neuropeptide FLP8 (VSHNNFLRF-amide).
OS   Macrobrachium rosenbergii (Giant fresh water prawn).
OC   Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC   Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Caridea;
OC   Palaemonoidea; Palaemonidae; Macrobrachium.
OX   NCBI_TaxID=79674;
RN   [1]
RP   SEQUENCE, AND MASS SPECTROMETRY.
RC   TISSUE=Eyestalk;
RX   MEDLINE=21107394; PubMed=11179812;
RA   Sithigorngul P., Saraithongkum W., Longyant S., Panchan N.,
RA   Sithigorngul W., Petsom A.;
RT   "Three more novel FMRFamide-like neuropeptide sequences from the
RT   eyestalk of the giant freshwater prawn Macrobrachium rosenbergii.";
RL   Peptides 22:191-197(2001).
CC   -!- MASS SPECTROMETRY: MW=1133.8; METHOD=MALDI.
CC   -!- SIMILARITY: Belongs to the FARP (FMRFamide related peptide)
CC       family.
DR   GO; GO:0007218; P:neuropeptide signaling pathway; IDA.
KW   Neuropeptide; Amidation.
FT   MOD_RES       9       9       AMIDATION.
SQ   SEQUENCE   9 AA;  1133 MW;  845A0729C44441F5 CRC64;

  Query Match             23.7%;  Score 14;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+05;
  Matches    2;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          9 HN 10
              ||
Db          3 HN 4
```

```
RESULT 14
UF02_MOUSE
ID   UF02_MOUSE     STANDARD;      PRT;     9 AA.
AC   P38640;
DT   01-OCT-1994 (Rel. 30, Created)
DT   01-OCT-1994 (Rel. 30, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Unknown protein from 2D-page of fibroblasts (P32) (Fragment).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Fibroblast;
RX   MEDLINE=95009907; PubMed=7523108;
RA   Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;
RT   "Separation and sequencing of familiar and novel murine proteins
RT   using preparative two-dimensional gel electrophoresis.";
RL   Electrophoresis 15:735-745(1994).
CC   -!- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
CC       protein is: 6.0, its MW is: 32 kDa.
FT   NON_TER       9       9
SQ   SEQUENCE   9 AA;  1102 MW;  7E73EAB6D05B1AAB CRC64;

  Query Match             23.7%;  Score 14;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+05;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
```

```
Qy          4 EIQ 6
              |||
Db          4 EIQ 6
```

```
RESULT 15
AL19_CARMA
ID   AL19_CARMA     STANDARD;      PRT;    10 AA.
AC   P81822;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   Carcinustatin 19.
OS   Carcinus maenas (Common shore crab) (Green crab).
OC   Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC   Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC   Eubrachyura; Portunoidea; Portunidae; Carcinus.
OX   NCBI_TaxID=6759;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Cerebral ganglion, and Thoracic ganglion;
RX   MEDLINE=98121193; PubMed=9461295;
RA   Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
RA   Thorpe A.;
RT   "Isolation and identification of multiple neuropeptides of the
RT   allatostatin superfamily in the shore crab Carcinus maenas.";
RL   Eur. J. Biochem. 250:727-734(1997).
CC   -!- FUNCTION: May act as a neurotransmitter or neuromodulator.
CC   -!- SIMILARITY: Belongs to the allatostatin family.
KW   Neuropeptide; Amidation; Multigene family.
FT   MOD_RES      10      10      AMIDATION (POTENTIAL).
SQ   SEQUENCE   10 AA;  1101 MW;  96687CD5AB569AB1 CRC64;

  Query Match             23.7%;  Score 14;  DB 1;  Length 10;
  Best Local Similarity   40.0%;  Pred. No. 7.2e+03;
  Matches    2;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          8 MHNLG 12
              |:: |
Db          5 MYSFG 9
```

```
Search completed: September  5, 2004, 09:35:02
Job time : 8.5 secs
```

This Page Blank (uspto)

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: September 5, 2004, 09:30:03 ; Search time 27.5 Seconds
(without alignments)
137.681 Million cell updates/sec

Title: US-09-730-174A-3
Perfect score: 59
Sequence: 1 SVSEIQLMHNLG 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 2565

Minimum DB seq length: 0
Maximum DB seq length: 12

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_25:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	27	45.8	11	13	Q9PS71	Q9ps71 agkistrodon
2	23	39.0	12	13	P82081	P82081 limnodynast
3	20	33.9	8	13	P82082	P82082 limnodynast
4	20	33.9	8	13	P82083	P82083 limnodynast
5	20	33.9	12	13	P82085	P82085 limnodynast
6	19	32.2	8	8	Q34909	Q34909 locusta mig
7	19	32.2	9	12	O92766	O92766 canine dist
8	19	32.2	9	12	O71066	O71066 canine dist
9	18	30.5	8	10	Q40659	Q40659 oryza sativ
10	18	30.5	10	12	Q9PXC3	Q9pxc3 hepatitis b
11	18	30.5	11	5	Q23876	Q23876 dictyosteli
12	18	30.5	12	15	Q85631	Q85631 avian carci
13	17	28.8	7	6	Q28742	Q28742 oryctolagus
14	17	28.8	9	4	Q15891	Q15891 homo sapien
15	17	28.8	9	8	Q9GD12	Q9gd12 linospadix
16	17	28.8	9	8	Q9GCV6	Q9gcv6 sclerosperm
17	17	28.8	11	8	Q35374	Q35374 paramecium
18	17	28.8	11	10	P82336	P82336 pisum sativ
19	17	28.8	11	13	Q9PST1	Q9pst1 fugu rubrip
20	16	27.1	7	13	Q8JJ20	Q8jj20 gallus gall
21	16	27.1	8	3	Q05403	Q05403 saccharomyc
22	16	27.1	8	4	Q15894	Q15894 homo sapien
23	16	27.1	9	2	Q44377	Q44377 aeromonas t
24	16	27.1	9	2	Q44468	Q44468 aeromonas v
25	16	27.1	9	2	Q8RKU3	Q8rku3 borrelia bu
26	16	27.1	9	2	Q43928	Q43928 aeromonas p
27	16	27.1	9	2	Q44001	Q44001 aeromonas e
28	16	27.1	9	2	Q9K4M6	Q9k4m6 staphylococ
29	16	27.1	9	10	Q9FXL0	Q9fxl0 lilium long
30	16	27.1	10	2	Q7WUG1	Q7wug1 pseudomonas
31	16	27.1	10	13	P82080	P82080 limnodynast
32	15	25.4	7	12	Q66205	Q66205 transmissib
33	15	25.4	8	13	P82079	P82079 limnodynast
34	15	25.4	9	2	Q43960	Q43960 azotobacter
35	15	25.4	9	5	Q8WTI9	Q8wti9 drosophila
36	15	25.4	10	6	Q9TS43	Q9ts43 sus scrofa
37	15	25.4	10	8	Q8WBR7	Q8wbr7 chaitophoru
38	15	25.4	10	11	Q61807	Q61807 mus musculu
39	15	25.4	11	6	Q9BDC8	Q9bdc8 pongo pygma
40	15	25.4	11	6	Q9BDQ9	Q9bdq9 gorilla gor
41	15	25.4	11	6	Q9BDD0	Q9bdd0 pan troglod
42	15	25.4	11	6	Q9BDC9	Q9bdc9 pan paniscu
43	15	25.4	12	2	Q9X6Y0	Q9x6y0 aquifex pyr
44	15	25.4	12	6	Q9TQY5	Q9tqy5 bos taurus
45	14	23.7	8	2	Q47273	Q47273 escherichia

ALIGNMENTS

RESULT 1
Q9PS71
ID Q9PS71 PRELIMINARY; PRT; 11 AA.
AC Q9PS71;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Fibrinolytic metalloproteinase (Fragment).
OS Agkistrodon contortrix.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Agkistrodon.
OX NCBI_TaxID=8720;
RN [1]
RP SEQUENCE.
RX MEDLINE=91378546; PubMed=1898066;
RA Guan A.L., Retzios A.D., Henderson G.N., Markland F.S.Jr.;
RT "Purification and characterization of a fibrinolytic enzyme from venom
RT of the southern copperhead snake (Agkistrodon contortrix
RT contortrix).";
RL Arch. Biochem. Biophys. 289:197-207(1991).
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1209 MW; 7CA02D1D41E8772B CRC64;

Query Match 45.8%; Score 27; DB 13; Length 11;
Best Local Similarity 71.4%; Pred. No. 1.4e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 6 QLMHNLG 12
:| ||||
Db 4 ELGHNLG 10

RESULT 2
P82081
ID P82081 PRELIMINARY; PRT; 12 AA.
AC P82081;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

```
DT   01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE   DYNASTIN 3.
OS   Limnodynastes terraereginae (Northen banjo frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Myobatrachidae;
OC   Limnodynastinae; Limnodynastes.
OX   NCBI_TaxID=104894;
RN   [1]
RP   SEQUENCE, AND MASS SPECTROMETRY.
RC   TISSUE=TIBIAL GLAND;
RA   Raftery M.J., Bradford A.M., Bowie J.H., Wallace J.C., Tyler M.J.;
RT   "Peptides from Australian frogs. The structure of the dynastins from
RT   the banjo frogs Limnodynastes interioras, Limnodynastes dumerilii and
RT   Limnodynastes terraereginae.";
RL   Aust. J. Chem. 46:833-842(1993).
CC   -!- MASS SPECTROMETRY: MW=1236; METHOD=FAB.
SQ   SEQUENCE   12 AA;  1236 MW;  147AA70FDF472724 CRC64;

  Query Match             39.0%;  Score 23;  DB 13;  Length 12;
  Best Local Similarity   66.7%;  Pred. No. 1e+03;
  Matches    4;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 LMHNLG 12
              |::|||
Db          6 LLNNLG 11


RESULT 3
P82082
ID   P82082      PRELIMINARY;      PRT;     8 AA.
AC   P82082;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE   DYNASTIN 4.
OS   Limnodynastes salmini (Salmin's-striped frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Myobatrachidae;
OC   Limnodynastinae; Limnodynastes.
OX   NCBI_TaxID=39404;
RN   [1]
RP   SEQUENCE, AND MASS SPECTROMETRY.
RC   TISSUE=SKIN SECRETION;
RA   Bradford A.M., Raftery M.J., Bowie J.H., Wallace J.C., Tyler M.J.;
RT   "Peptides from Australian frogs. The structure of the dynastins from
RT   Limnodynastes salmini and Fletcherin from Limnodynastes fletcheri.";
RL   Aust. J. Chem. 46:1235-1244(1993).
CC   -!- MASS SPECTROMETRY: MW=772; METHOD=FAB.
SQ   SEQUENCE   8 AA;  772 MW;  7B58772455A2C728 CRC64;

  Query Match             33.9%;  Score 20;  DB 13;  Length 8;
  Best Local Similarity   66.7%;  Pred. No. 1e+06;
  Matches    4;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 LMHNLG 12
              |: |||
Db          2 LVSNLG 7


RESULT 4
P82083
ID   P82083      PRELIMINARY;      PRT;     8 AA.
AC   P82083;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE   DYNASTIN 5.
OS   Limnodynastes salmini (Salmin's-striped frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Myobatrachidae;
OC   Limnodynastinae; Limnodynastes.
OX   NCBI_TaxID=39404;
RN   [1]
RP   SEQUENCE, AND MASS SPECTROMETRY.
RC   TISSUE=SKIN SECRETION;
RA   Bradford A.M., Raftery M.J., Bowie J.H., Wallace J.C., Tyler M.J.;
RT   "Peptides from Australian frogs. The structure of the dynastins from
RT   Limnodynastes salmini and Fletcherin from Limnodynastes fletcheri.";
RL   Aust. J. Chem. 46:1235-1244(1993).
CC   -!- MASS SPECTROMETRY: MW=786; METHOD=FAB.
SQ   SEQUENCE   8 AA;  786 MW;  7B58772455B05728 CRC64;

  Query Match             33.9%;  Score 20;  DB 13;  Length 8;
  Best Local Similarity   66.7%;  Pred. No. 1e+06;
  Matches    4;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 LMHNLG 12
              |: |||
Db          2 LISNLG 7


RESULT 5
P82085
ID   P82085      PRELIMINARY;      PRT;     12 AA.
AC   P82085;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE   DYNASTIN 7.
OS   Limnodynastes salmini (Salmin's-striped frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Myobatrachidae;
OC   Limnodynastinae; Limnodynastes.
OX   NCBI_TaxID=39404;
RN   [1]
RP   SEQUENCE, AND MASS SPECTROMETRY.
RC   TISSUE=SKIN SECRETION;
RA   Bradford A.M., Raftery M.J., Bowie J.H., Wallace J.C., Tyler M.J.;
RT   "Peptides from Australian frogs. The structure of the dynastins from
RT   Limnodynastes salmini and Fletcherin from Limnodynastes fletcheri.";
RL   Aust. J. Chem. 46:1235-1244(1993).
CC   -!- MASS SPECTROMETRY: MW=1114; METHOD=FAB.
SQ   SEQUENCE   12 AA;  1114 MW;  3AB5A976CAA72728 CRC64;

  Query Match             33.9%;  Score 20;  DB 13;  Length 12;
  Best Local Similarity   66.7%;  Pred. No. 4.3e+03;
  Matches    4;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 LMHNLG 12
              |: |||
Db          6 LLTNLG 11


RESULT 6
Q34909
ID   Q34909      PRELIMINARY;      PRT;     8 AA.
AC   Q34909;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Cytochrome b (Fragment).
OS   Locusta migratoria (Migratory locust).
OG   Mitochondrion.
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
OC   Acridoidea; Acrididae; Oedipodinae; Locusta.
OX   NCBI_TaxID=7004;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=88223478; PubMed=2836084;
RA   McCracken A., Uhlenbusch I., Gellissen G.;
RT   "Structure of the cloned Locusta migratoria mitochondrial genome:
RT   restriction mapping and sequence of its ND-1(URF-1) gene.";
RL   Curr. Genet. 11:625-630(1987).
DR   EMBL; X05286; CAA28905.1; -.
DR   GO; GO:0005739; C:mitochondrion; IEA.
```

```
KW   Mitochondrion.
FT   NON_TER       1      1
FT   NON_TER       8      8
SQ   SEQUENCE   8 AA;  1019 MW;  F8E33723304B45B6 CRC64;

  Query Match             32.2%;  Score 19;  DB 8;  Length 8;
  Best Local Similarity   50.0%;  Pred. No. 1e+06;
  Matches    4;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 VSEIQLMH 9
              :| |:| |
Db          1 MSYIKLKH 8


RESULT 7
O92766
ID   O92766      PRELIMINARY;      PRT;     9 AA.
AC   O92766;
DT   01-NOV-1998 (TrEMBLrel. 08, Created)
DT   01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT   01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE   Fusion protein (Fragment).
GN   F.
OS   Canine distemper virus.
OC   Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC   Paramyxoviridae; Paramyxovirinae; Morbillivirus.
OX   NCBI_TaxID=11232;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Dog #5526/89;
RA   Liermann H., Harder T., Haas L.;
RT   "Genetic analysis of the central untranslated genome region and the
RT   proximal coding part of the F gene of wild-type and vaccine distemper
RT   morbilliviruses.";
RL   Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF026237; AAC09167.1; -.
FT   NON_TER       9      9
SQ   SEQUENCE   9 AA;  1011 MW;  F281732760533441 CRC64;

  Query Match             32.2%;  Score 19;  DB 12;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 1e+06;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 MHN 10
              |||
Db          1 MHN 3


RESULT 8
O71066
ID   O71066      PRELIMINARY;      PRT;     9 AA.
AC   O71066;
DT   01-AUG-1998 (TrEMBLrel. 07, Created)
DT   01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   Fusion protein (Fragment).
GN   F.
OS   Canine distemper virus.
OC   Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC   Paramyxoviridae; Paramyxovirinae; Morbillivirus.
OX   NCBI_TaxID=11232;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Dog #10757/96;
RA   Liermann H., Harder T., Haas L.;
RT   "Genetic analysis of the central untranslated genome region and the
RT   proximal coding part of the F gene of wild-type and vaccine distemper
RT   morbilliviruses.";
RL   Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF026234; AAC09164.1; -.
FT   NON_TER       9      9
SQ   SEQUENCE   9 AA;  1124 MW;  F29D045760440441 CRC64;

  Query Match             32.2%;  Score 19;  DB 12;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 1e+06;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 MHN 10
              |||
Db          1 MHN 3


RESULT 9
Q40659
ID   Q40659      PRELIMINARY;      PRT;     8 AA.
AC   Q40659;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE   Alpha-amylase (Fragment).
OS   Oryza sativa (Rice).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC   Ehrhartoideae; Oryzeae; Oryza.
OX   NCBI_TaxID=4530;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91078641; PubMed=2258052;
RA   Kumagai M.H., Shah M., Terashima M., Vrkljan Z., Whitaker J.R.,
RA   Rodriquez R.L.;
RT   "Expression and secretion of rice alpha-amylase by saccharomycers
RT   cerevisiae.";
RL   Gene 94:209-216(1990).
DR   EMBL; M62916; AAA33892.1; -.
DR   Gramene; Q40659; -.
FT   NON_TER       8      8
SQ   SEQUENCE   8 AA;  948 MW;  EBC694444732D6D6 CRC64;

  Query Match             30.5%;  Score 18;  DB 10;  Length 8;
  Best Local Similarity   28.6%;  Pred. No. 1e+06;
  Matches    2;  Conservative    5;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 IQLMHNL 11
              :|:::|:
Db          1 MQVLNNM 7


RESULT 10
Q9PXC3
ID   Q9PXC3      PRELIMINARY;      PRT;    10 AA.
AC   Q9PXC3;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   E antigen P20E (Fragment).
OS   Hepatitis B virus.
OC   Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX   NCBI_TaxID=10407;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=92013147; PubMed=1717588;
RA   Takahashi K., Kishimoto S., Ohori K., Yoshizawa H., Machida A.,
RA   Ohnuma H., Tsuda F., Munekata E., Miyakawa Y., Mayumi M.;
RT   "Molecular heterogeneity of e antigen polypeptides in sera from
RT   carriers of hepatitis B virus.";
RL   J. Immunol. 147:3156-3160(1991).
DR   PIR; B46453; B46453.
FT   NON_TER      10     10
SQ   SEQUENCE   10 AA;  1238 MW;  485A6E3AE721E9C7 CRC64;

  Query Match             30.5%;  Score 18;  DB 12;  Length 10;
  Best Local Similarity   60.0%;  Pred. No. 9.1e+03;
  Matches    3;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          5 IQLMH 9
              :|| |
```

```
Db          1 MQLFH 5


RESULT 11
Q23876
ID   Q23876      PRELIMINARY;      PRT;    11 AA.
AC   Q23876;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE   Actin 4.
OS   Dictyostelium discoideum (Slime mold).
OC   Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
OX   NCBI_TaxID=44689;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=82260445; PubMed=6286214;
RA   McKeown M., Firtel R.A.;
RT   "Actin multigene family of Dictyostelium.";
RL   Cold Spring Harb. Symp. Quant. Biol. 46:495-505(1982).
DR   EMBL; K02957; AAA33150.1; -.
DR   EMBL; K02956; AAA33150.1; JOINED.
SQ   SEQUENCE   11 AA;  1205 MW;  728B4C14C6C2CAAB CRC64;

  Query Match             30.5%;  Score 18;  DB 5;  Length 11;
  Best Local Similarity   28.6%;  Pred. No. 1e+04;
  Matches    2;  Conservative    4;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 EIQLMHN 10
              ::| ::|
Db          5 DVQALNN 11


RESULT 12
Q85631
ID   Q85631      PRELIMINARY;      PRT;    12 AA.
AC   Q85631;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   MH2, proviral DNA, myc to 3' LTR (Fragment).
OS   Avian carcinoma virus.
OC   Viruses; Retroid viruses; Retroviridae; Alpharetrovirus.
OX   NCBI_TaxID=11958;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=85033920; PubMed=6092695;
RA   Sutrave P., Jansen H.W., Bister K., Rapp U.R.;
RT   "3'-terminal region of avian carcinoma virus MH2 shares sequence
RT   elements with avian sarcoma viruses Y73 and SR-A.";
RL   J. Virol. 52:703-705(1984).
DR   EMBL; K03100; AAA42388.1; -.
FT   NON_TER       1      1
SQ   SEQUENCE   12 AA;  1466 MW;  72E4B884F30736DB CRC64;

  Query Match             30.5%;  Score 18;  DB 15;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+04;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          9 HNL 11
              |||
Db          2 HNL 4


RESULT 13
Q28742
ID   Q28742      PRELIMINARY;      PRT;     7 AA.
AC   Q28742;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Alpha-myosin heavy chain (Fragment).
OS   Oryctolagus cuniculus (Rabbit).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX   NCBI_TaxID=9986;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=84221901; PubMed=6328491;
RA   Friedman D.J., Umeda P.K., Sinha A.M., Hsu H.-J., Jokovcic S.,
RA   Rabinowitz M.;
RT   "Characterization of genomic clones specifying rabbit alpha- and beta-
RT   ventricular myosin heavy chains.";
RL   Proc. Natl. Acad. Sci. U.S.A. 81:3044-3048(1984).
DR   EMBL; K01698; AAA31415.1; -.
DR   PIR; I46868; I46868.
FT   NON_TER       1      1
SQ   SEQUENCE   7 AA;  916 MW;  6B1B1AA1E69326B0 CRC64;

  Query Match             28.8%;  Score 17;  DB 6;  Length 7;
  Best Local Similarity   60.0%;  Pred. No. 1e+06;
  Matches    3;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          6 QLMHN 10
              | ||:
Db          1 QKMHD 5


RESULT 14
Q15891
ID   Q15891      PRELIMINARY;      PRT;     9 AA.
AC   Q15891;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   (Clone XP2E8B) (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Placenta;
RA   Lee C.-C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M.,
RA   Coolbaugh M.I., Chinault C.A., Baldini A., Lindsay E.A., Zhao Z.-Y.,
RA   Caskey C.T.H.;
RT   "Isolation of chromosome-specific genes by reciprocal probing of
RT   arrayed cDNAs and cosmid libraries.";
RL   Hum. Mol. Genet. 0:0-0(1995).
DR   EMBL; L32131; AAA73881.1; -.
FT   NON_TER       1      1
FT   NON_TER       9      9
SQ   SEQUENCE   9 AA;  1030 MW;  E56635A1A33686D1 CRC64;

  Query Match             28.8%;  Score 17;  DB 4;  Length 9;
  Best Local Similarity   44.4%;  Pred. No. 1e+06;
  Matches    4;  Conservative    2;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          4 EIQLMHNLG 12
              | |:  :||
Db          1 EHQMKTSLG 9


RESULT 15
Q9GD12
ID   Q9GD12      PRELIMINARY;      PRT;     9 AA.
AC   Q9GD12;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Ribosomal protein S16 (Fragment).
GN   RPS16.
OS   Linospadix monostachya.
OG   Chloroplast.
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; Liliopsida; Arecaceae; Arecoideae;
```

```
OC   Areceae; Linospadicinae; Linospadix.
OX   NCBI_TaxID=131282;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Leaf;
RA   Asmussen C.B., Chase M.W.;
RT   "Coding and noncoding plastid DNA in palm systematics.";
RL   Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AJ404941; CAC17917.1; -.
DR   GO; GO:0009507; C:chloroplast; IEA.
KW   Chloroplast.
FT   NON_TER       1      1
FT   NON_TER       9      9
SQ   SEQUENCE   9 AA;  1106 MW;  1B9236C2C0441B50 CRC64;

  Query Match             28.8%;  Score 17;  DB 8;  Length 9;
  Best Local Similarity   75.0%;  Pred. No. 1e+06;
  Matches    3;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 IQLM 8
              :|||
Db          6 VQLM 9


Search completed: September  5, 2004, 09:36:59
Job time : 29.5 secs
```

This page blank (uspto)

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: September 5, 2004, 09:26:47 ; Search time 36.5 Seconds
(without alignments)
92.892 Million cell updates/sec

Title: US-09-730-174A-3
Perfect score: 59
Sequence: 1 SVSEIQLMHNLG 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 368311

Minimum DB seq length: 0
Maximum DB seq length: 12

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	50	84.7	11	3	AAY96968	Aay96968 Parathyro
2	50	84.7	11	6	ABG72607	Abg72607 Parathyro
3	50	84.7	12	6	ABG72608	Abg72608 Parathyro
4	49	83.1	10	2	AAR91644	Aar91644 Human par
5	49	83.1	10	3	AAY68767	Aay68767 Amino aci
6	49	83.1	10	4	AAB86219	Aab86219 Human par
7	49	83.1	10	6	ABR44166	Abr44166 Human par
8	45	76.3	9	4	AAB86225	Aab86225 Human par
9	43	72.9	9	2	AAR91645	Aar91645 Human par
10	43	72.9	9	3	AAY96981	Aay96981 Parathyro
11	43	72.9	9	4	AAB86220	Aab86220 Human par
12	40.5	68.6	11	2	AAY50600	Aay50600 Resin bou
13	40	67.8	9	3	AAB01862	Aab01862 PTH(1-14)
14	40	67.8	9	3	AAY96966	Aay96966 Parathyro
15	37	62.7	9	3	AAB01863	Aab01863 PTH(1-14)
16	37	62.7	10	4	AAB96932	Aab96932 Rat parat
17	37	62.7	11	4	AAB96931	Aab96931 Rat parat
18	37	62.7	11	4	AAB96915	Aab96915 Parathyro
19	37	62.7	11	4	AAB84770	Aab84770 Parathyro
20	37	62.7	12	4	AAB96914	Aab96914 Parathyro
21	37	62.7	12	4	AAB84769	Aab84769 Parathyro
22	36	61.0	9	3	AAY78849	Aay78849 Parathyro
23	35	59.3	8	2	AAR91646	Aar91646 Human par
24	35	59.3	8	3	AAB07467	Aab07467 Antigenic
25	35	59.3	8	4	AAB86221	Aab86221 Human par
26	35	59.3	10	6	ABP71484	Abp71484 Parathyro
27	35	59.3	11	6	ABP71485	Abp71485 Parathyro
28	35	59.3	11	6	ABP71483	Abp71483 Parathyro
29	35	59.3	12	2	AAW45785	Aaw45785 Parathyro
30	35	59.3	12	6	ABP71482	Abp71482 Parathyro
31	33	55.9	9	3	AAB01866	Aab01866 PTH(1-14)
32	32	54.2	11	1	AAP82547	Aap82547 (Asn10, T
33	32	54.2	11	4	AAB96892	Aab96892 Rat parat
34	32	54.2	12	4	AAB96891	Aab96891 Rat parat
35	30	50.8	7	2	AAR91647	Aar91647 Human par
36	30	50.8	7	4	AAB86222	Aab86222 Human par
37	30	50.8	9	3	AAB01864	Aab01864 PTH(1-14)
38	30	50.8	9	3	AAY97062	Aay97062 PTH-rP N-
39	29	49.2	10	5	ABG69386	Abg69386 Vascular
40	29	49.2	12	5	AAU93357	Aau93357 Granulocy
41	27	45.8	11	4	ABU54029	Abu54029 Human DNA
42	27	45.8	12	2	AAR89301	Aar89301 Japanese
43	27	45.8	12	3	AAB21270	Aab21270 Fertilin
44	26	44.1	6	2	AAR91648	Aar91648 Human par
45	26	44.1	6	3	AAY68764	Aay68764 Amino aci

ALIGNMENTS

RESULT 1
AAY96968
ID AAY96968 standard; peptide; 11 AA.
XX
AC AAY96968;
XX
DT 31-OCT-2000 (first entry)
XX
DE Parathyroid hormone N-terminal signaling domain (residues 1-11).
XX
KW PTH; parathyroid hormone; N-terminal; signaling domain; bone mass;
KW bone reformation; resorption; remodeling; tether1; osteoporosis.
XX
OS Homo sapiens.
XX
PN WO200039278-A2.
XX
PD 06-JUL-2000.
XX
PF 30-DEC-1999; 99WO-US031108.
XX
PR 31-DEC-1998; 98US-0114577P.
XX
PA (GARD/) GARDELLA T J.
PA (KRON/) KRONENBERG H M.
PA (POTT/) POTTS J T.
PA (JUEP/) JUEPPNER H.
XX
PI Gardella TJ, Kronenberg HM, Potts JT, Jueppner H;
XX
DR WPI; 2000-452384/39.
XX
PT New compound comprising an amino terminal signaling functional domain
PT linked to a carboxy-terminal binding portion of parathyroid hormone for
PT treating mammalian conditions characterized by decreases in bone mass.
XX
PS Claim 4; Page 92; 119pp; English.
XX
CC Compounds of the structure or formula S-(L)_n-B, R_1-S-(L)_n-R or S-(L)_n
CC -R, are new. S is an amino terminal signaling functional domain of
CC parathyroid hormone (PTH); L is a linker molecule present n times (where
CC n is a positive integer 1-10 (preferably 4)); B is a C-terminal binding
CC portion of PTH(1-34) or a PTH-related protein (PTH-rP) (1-34); R_1 is the
CC PTH-1 receptor signal sequence; and R is (a portion of) PTH-1 receptor
CC sequence. The new compounds are used for treating mammalian conditions
CC characterized by decreases in bone mass, determining rates of bone
CC reformation, bone resorption and/or bone remodeling, treating diseases
CC and disorders associated with decreased tether1 activity, increasing cAMP

```
CC   in a mammalian cell having PTH-1 receptors, or screening for a peptide or
CC   non-peptide PTH (claimed). The new compound can be administered by
CC   inhalation unlike the large native PTH or PTHrP which avoids the need for
CC   regular injections to treat osteoporosis
XX
SQ   Sequence 11 AA;

  Query Match             84.7%;  Score 50;  DB 3;  Length 11;
  Best Local Similarity   90.9%;  Pred. No. 0.012;
  Matches   10;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SVSEIQLMHNL 11
              :||||||||||
Db          1 AVSEIQLMHNL 11


RESULT 2
ABG72607
ID   ABG72607 standard; peptide; 11 AA.
XX
AC   ABG72607;
XX
DT   11-FEB-2003  (first entry)
XX
DE   Parathyroid hormone antigenic peptide 2-12.
XX
KW   Human; parathyroid hormone; antigen; hypercalcaemia; osteoporosis;
KW   primary hyperparathyroidism; mouse; rat; bovine; porcine; canine.
XX
OS   Homo sapiens.
OS   Mus sp.
OS   Rattus sp.
OS   Bos taurus.
OS   Sus scrofa.
OS   Canis familiaris.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 6
FT                   /label= Leu, Phe
XX
PN   US2002110871-A1.
XX
PD   15-AUG-2002.
XX
PF   05-DEC-2000; 2000US-00730174.
XX
PR   05-DEC-2000; 2000US-00730174.
XX
PA   (ZAHR/) ZAHRADNIK R J.
PA   (LAVI/) LAVIGNE J R.
XX
PI   Zahradnik RJ,  Lavigne JR;
XX
DR   WPI; 2003-066685/06.
XX
PT   New parathyroid hormone (PTH) antigenic peptide inducing the formation
PT   and isolation of antibodies having an affinity to it, useful for
PT   determining bioactive PTH levels in serum, plasma and/or cell culture
PT   media.
XX
PS   Claim 1; Page 5; 11pp; English.
XX
CC   The invention relates to a new antigenic peptide for inducing the
CC   formation and isolation of antibodies having an affinity to it, being
CC   formed from the N-terminus of parathyroid hormone (PTH). Also included
CC   are; (1) a method for producing antibodies useful in the determination of
CC   PTH levels in a biological sample comprising: (a) providing at least one
CC   first peptide antigen comprising a peptide fragment of PTH; (b)
CC   administering the first peptide antigen to a host animal to induce
CC   antibody production; (c) monitoring the antibody titre produced; (d)
CC   isolating antisera produced in the host animal; and (e) selecting
CC   antisera from the isolated antisera produced in the host that is capable
CC   of binding to a second peptide antigen; (2) an antibody (ab) produced by
CC   the method; and (3) test kits and analytical procedures used for the
CC   determination of bioactive intact PTH utilising (ab). The methods and
CC   compositions of the present invention are useful for determining
CC   bioactive intact PTH levels in serum, plasma and/or cell culture media.
CC   The antigens, antibodies and methods of the present invention, as
CC   compared to prior art, have the particular advantages of possessing
CC   greater affinity for PTH, and in particular, are designed to have a novel
CC   recognition for amino acid residues extending beyond the first N-terminal
CC   PTH residue, and further have negligible cross-reactivity with the large
CC   non-molecular forms of PTH. PTH levels are an important parameter in
CC   patients suffering from hypercalcaemia, osteoporosis and primary
CC   hyperparathyroidism. The present sequence represents a PTH antigenic
CC   peptide representing amino acids 2-12 of human, mouse, rat, porcine,
CC   canine and bovine PTH
XX
SQ   Sequence 11 AA;

  Query Match             84.7%;  Score 50;  DB 6;  Length 11;
  Best Local Similarity   90.9%;  Pred. No. 0.012;
  Matches   10;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 VSEIQLMHNLG 12
              ||||| |||||
Db          1 VSEIQXMHNLG 11


RESULT 3
ABG72608
ID   ABG72608 standard; peptide; 12 AA.
XX
AC   ABG72608;
XX
DT   11-FEB-2003  (first entry)
XX
DE   Parathyroid hormone antigenic peptide 1-12.
XX
KW   Human; parathyroid hormone; antigen; hypercalcaemia; osteoporosis;
KW   primary hyperparathyroidism; mouse; rat; bovine; porcine; canine.
XX
OS   Homo sapiens.
OS   Mus sp.
OS   Rattus sp.
OS   Bos taurus.
OS   Sus scrofa.
OS   Canis familiaris.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 1
FT                   /label= Ser, Ala
FT   Misc-difference 7
FT                   /label= Leu, Phe
XX
PN   US2002110871-A1.
XX
PD   15-AUG-2002.
XX
PF   05-DEC-2000; 2000US-00730174.
XX
PR   05-DEC-2000; 2000US-00730174.
XX
PA   (ZAHR/) ZAHRADNIK R J.
PA   (LAVI/) LAVIGNE J R.
XX
PI   Zahradnik RJ,  Lavigne JR;
XX
DR   WPI; 2003-066685/06.
XX
PT   New parathyroid hormone (PTH) antigenic peptide inducing the formation
PT   and isolation of antibodies having an affinity to it, useful for
PT   determining bioactive PTH levels in serum, plasma and/or cell culture
PT   media.
XX
PS   Claim 2; Page 5; 11pp; English.
```

```
XX
CC   The invention relates to a new antigenic peptide for inducing the
CC   formation and isolation of antibodies having an affinity to it, being
CC   formed from the N-terminus of parathyroid hormone (PTH). Also included
CC   are; (1) a method for producing antibodies useful in the determination of
CC   PTH levels in a biological sample comprising: (a) providing at least one
CC   first peptide antigen comprising a peptide fragment of PTH; (b)
CC   administering the first peptide antigen to a host animal to induce
CC   antibody production; (c) monitoring the antibody titre produced; (d)
CC   isolating antisera produced in the host animal; and (e) selecting
CC   antisera from the isolated antisera produced in the host that is capable
CC   of binding to a second peptide antigen; (2) an antibody (ab) produced by
CC   the method; and (3) test kits and analytical procedures used for the
CC   determination of bioactive intact PTH utilising (ab). The methods and
CC   compositions of the present invention are useful for determining
CC   bioactive intact PTH levels in serum, plasma and/or cell culture media.
CC   The antigens, antibodies and methods of the present invention, as
CC   compared to prior art, have the particular advantages of possessing
CC   greater affinity for PTH, and in particular, are designed to have a novel
CC   recognition for amino acid residues extending beyond the first N-terminal
CC   PTH residue, and further have negligible cross-reactivity with the large
CC   non-molecular forms of PTH. PTH levels are an important parameter in
CC   patients suffering from hypercalcaemia, osteoporosis and primary
CC   hyperparathyroidism. The present sequence represents a PTH antigenic
CC   peptide representing amino acids 1-12 of human, mouse, rat, porcine,
CC   canine and bovine PTH
XX
SQ   Sequence 12 AA;

  Query Match             84.7%;  Score 50;  DB 6;  Length 12;
  Best Local Similarity   90.9%;  Pred. No. 0.014;
  Matches   10;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 VSEIQLMHNLG 12
              ||||| |||||
Db          2 VSEIQXMHNLG 12


RESULT 4
AAR91644
ID   AAR91644 standard; peptide; 10 AA.
XX
AC   AAR91644;
XX
DT   06-NOV-1996  (first entry)
XX
DE   Human parathyroid hormone antigenic peptide hPTH 1-10.
XX
KW   Human parathyroid hormone; hPTH; antigen; alpha-helix; immunogen;
KW   diagnosis; active hPTH 1-37.
XX
OS   Synthetic.
XX
PN   DE4434551-A1.
XX
PD   04-APR-1996.
XX
PF   28-SEP-1994;   94DE-04434551.
XX
PR   28-SEP-1994;   94DE-04434551.
XX
PA   (FORS/) FORSSMANN W.
XX
PI   Adermann K,  Forssmann W,  Hock D,  Maegerlein M;
XX
DR   WPI; 1996-180391/19.
XX
PT   New antigenic peptide(s) from human parathyroid hormone - and antibodies
PT   generated using them, able to distinguish between active and inactive
PT   forms of the hormone.
XX
PS   Claim 2; Page 4; 5pp; German.
XX
CC   The present sequence is a specific example of claimed immunogenic
CC   peptides having a sequence from hPTH(1-37) which includes the N- or C-
CC   terminal alpha-helical region and/or the non-structured region of the
CC   hormone. Antibodies and their binding fragments generated by injecting an
CC   animal with the peptides are useful as diagnostic reagents for
CC   determination of biologically active hPTH(1-37)
XX
SQ   Sequence 10 AA;

  Query Match             83.1%;  Score 49;  DB 2;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0.017;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SVSEIQLMHN 10
              ||||||||||
Db          1 SVSEIQLMHN 10


RESULT 5
AAY68767
ID   AAY68767 standard; peptide; 10 AA.
XX
AC   AAY68767;
XX
DT   05-MAY-2000  (first entry)
XX
DE   Amino acids 1-10 of a parathyroid hormone (pTH).
XX
KW   Parathyroid hormone; lipolysis; cosmetic; dermatological; skin care;
KW   slimming treatment; cellulite; skin firming.
XX
OS   Unidentified.
XX
PN   WO200004047-A1.
XX
PD   27-JAN-2000.
XX
PF   07-JUL-1999;   99WO-FR001687.
XX
PR   17-JUL-1998;   98FR-00009193.
XX
PA   (SEDE-) SEDERMA.
XX
PI   Lintner K;
XX
DR   WPI; 2000-171243/15.
XX
PT   New parathyroid hormone fragment peptides, used as lipolysis stimulants
PT   in topically applied cosmetic compositions for slimming treatment of
PT   excessive weight in hips and thighs.
XX
PS   Claim 1; Page 8; 18pp; French.
XX
CC   The present sequence represents a parathyroid hormone (pTH) fragment,
CC   comprising amino acids 1-10. Parathyroid hormone fragments of the
CC   invention have lipolysis stimulating activity (especially when topically
CC   administered). The lipolytic activity of the peptides is enhanced when
CC   they are chemically modified to increase their lipophilicity. The
CC   peptides are used in cosmetic or dermatological compositions for skin
CC   care. They are especially used for slimming treatment of excessive weight
CC   in the thighs and hips, in the treatment of cellulite and for skin
CC   firming
XX
SQ   Sequence 10 AA;

  Query Match             83.1%;  Score 49;  DB 3;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0.017;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SVSEIQLMHN 10
              ||||||||||
Db          1 SVSEIQLMHN 10
```

RESULT 6
AAB86219
ID AAB86219 standard; peptide; 10 AA.
XX
AC AAB86219;
XX
DT 03-SEP-2001 (first entry)
XX
DE Human parathyroid hormone immunogenic peptide SEQ ID 1.
XX
KW Parathyroid hormone; hPTH; immunogenic peptide; human; epitope;
KW diagnosis; calcium-metabolism disorder; osteopathy; antagonist;
KW hypo-parathyroidism; hyper-parathyroidism.
XX
OS Homo sapiens.
XX
PN DE19961350-A1.
XX
PD 21-JUN-2001.
XX
PF 17-DEC-1999; 99DE-01061350.
XX
PR 17-DEC-1999; 99DE-01061350.
XX
PA (IMMU-) IMMUNDIAGNOSTIK AG.
XX
PI Armbruster FP;
XX
DR WPI; 2001-376318/40.
XX
PT Determining the content of physiologically active parathyroid hormone,
PT useful in diagnosis of calcium-metabolism disorders, using two antibodies
PT reactive with different epitopes.
XX
PS Disclosure; Page 3; 10pp; German.
XX
CC This invention describes a novel method for determining (M1) the content
CC of active parathyroid hormone (A) by treating a sample with (i) antibody
CC (Ab1) that recognizes the epitope formed by amino acids (aa) 1-3 of (A),
CC and including the N-terminal residue and (ii) antibody (Ab2) that
CC recognizes an epitope within the receptor-binding site of (A). The number
CC of molecules that react with both antibodies is determined and used to
CC calculate the content of physiologically active (A). The method is used
CC for diagnosis of calcium-metabolism disorders, osteopathy, or hypo- or
CC hyper-parathyroidism. The method (unlike known assays) recognizes that
CC (i) some fragments of (A) shorter than the complete (84 aa) peptide are
CC active and (ii) that apparently intact peptide may be biologically
CC inactive, and also takes into account the fact that some fragments of (A)
CC are antagonistic (these have the receptor-binding site but lack the N-
CC terminus). It thus provides a true measure of the content of
CC physiologically active (A); contrast methods that measure intact peptide
CC and its 1-37 fragment which may produce falsely high values. This
CC sequence represents a peptide fragment used to illustrate the method of
CC the invention
XX
SQ Sequence 10 AA;

Query Match 83.1%; Score 49; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHN 10
||||||||||
Db 1 SVSEIQLMHN 10

RESULT 7
ABR44166
ID ABR44166 standard; peptide; 10 AA.
XX
AC ABR44166;
XX
DT 04-AUG-2003 (first entry)
XX
DE Human parathyroid hormone (hPTH) fragment (residues 1-10).
XX
KW Fusion peptide; tat; hPTHDP; parathyroid hormone; skin; cosmetic;
KW lipolysis; human; hPTH.
XX
OS Homo sapiens.
XX
PN WO2003035697-A1.
XX
PD 01-MAY-2003.
XX
PF 06-MAY-2002; 2002WO-KR000835.
XX
PR 27-SEP-2001; 2001KR-00060245.
PR 15-MAR-2002; 2002KR-00014062.
XX
PA (GLDS) LG HOUSEHOLD & HEALTH CARE LTD.
XX
PI Song Y, Kang N, Park S, Cho W, Kang S, Lee Y, Lim J, Min H;
PI Chang M;
XX
DR WPI; 2003-468288/44.
XX
PT Novel fusion peptide comprising self cell-penetrating Tat peptide bound
PT to human parathyroid hormone-derived peptide, useful as component of skin
PT slimming cosmetic composition.
XX
PS Claim 5; Page 6; 32pp; English.
XX
CC The invention relates to a fusion peptide (Tat-hPTHDP), where self cell-
CC penetrating Tat peptide is bound to human parathyroid hormone-derived
CC peptide (hPTHDP). The fusion peptide is useful as a component of skin
CC slimming cosmetic composition. The fusion peptide does not cause
CC irritation, easily and safely penetrates into integument and endothelium,
CC does not cause skin disease and has superior lipolysis effects, and is
CC durable. The present sequence represents a human parathyroid hormone
CC (hPTH) fragment that can be used to construct the fusion peptide
XX
SQ Sequence 10 AA;

Query Match 83.1%; Score 49; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHN 10
||||||||||
Db 1 SVSEIQLMHN 10

RESULT 8
AAB86225
ID AAB86225 standard; peptide; 9 AA.
XX
AC AAB86225;
XX
DT 03-SEP-2001 (first entry)
XX
DE Human parathyroid hormone immunogenic peptide SEQ ID 7.
XX
KW Parathyroid hormone; hPTH; immunogenic peptide; human; epitope;
KW diagnosis; calcium-metabolism disorder; osteopathy; antagonist;
KW hypo-parathyroidism; hyper-parathyroidism.
XX
OS Homo sapiens.
XX
PN DE19961350-A1.
XX
PD 21-JUN-2001.
XX
PF 17-DEC-1999; 99DE-01061350.
XX

PR 17-DEC-1999; 99DE-01061350.
XX
PA (IMMU-) IMMUNDIAGNOSTIK AG.
XX
PI Armbruster FP;
XX
DR WPI; 2001-376318/40.
XX
PT Determining the content of physiologically active parathyroid hormone,
PT useful in diagnosis of calcium-metabolism disorders, using two antibodies
PT reactive with different epitopes.
XX
PS Disclosure; Page 3; 10pp; German.
XX
CC This invention describes a novel method for determining (M1) the content
CC of active parathyroid hormone (A) by treating a sample with (i) antibody
CC (Ab1) that recognizes the epitope formed by amino acids (aa) 1-3 of (A),
CC and including the N-terminal residue and (ii) antibody (Ab2) that
CC recognizes an epitope within the receptor-binding site of (A). The number
CC of molecules that react with both antibodies is determined and used to
CC calculate the content of physiologically active (A). The method is used
CC for diagnosis of calcium-metabolism disorders, osteopathy, or hypo- or
CC hyper-parathyroidism. The method (unlike known assays) recognizes that
CC (i) some fragments of (A) shorter than the complete (84 aa) peptide are
CC active and (ii) that apparently intact peptide may be biologically
CC inactive, and also takes into account the fact that some fragments of (A)
CC are antagonistic (these have the receptor-binding site but lack the N-
CC terminus). It thus provides a true measure of the content of
CC physiologically active (A); contrast methods that measure intact peptide
CC and its 1-37 fragment which may produce falsely high values. This
CC sequence represents a peptide fragment used to illustrate the method of
CC the invention
XX
SQ Sequence 9 AA;

Query Match 76.3%; Score 45; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VSEIQLMHN 10
|||||||||
Db 1 VSEIQLMHN 9

RESULT 9
AAR91645
ID AAR91645 standard; peptide; 9 AA.
XX
AC AAR91645;
XX
DT 06-NOV-1996 (first entry)
XX
DE Human parathyroid hormone antigenic peptide hPTH 1-9.
XX
KW Human parathyroid hormone; hPTH; antigen; alpha-helix; immunogen;
KW diagnosis; active hPTH 1-37.
XX
OS Synthetic.
XX
PN DE4434551-A1.
XX
PD 04-APR-1996.
XX
PF 28-SEP-1994; 94DE-04434551.
XX
PR 28-SEP-1994; 94DE-04434551.
XX
PA (FORS/) FORSSMANN W.
XX
PI Adermann K, Forssmann W, Hock D, Maegerlein M;
XX
DR WPI; 1996-180391/19.
XX
PT New antigenic peptide(s) from human parathyroid hormone - and antibodies
PT generated using them, able to distinguish between active and inactive
PT forms of the hormone.
XX
PS Claim 2; Page 4; 5pp; German.
XX
CC The present sequence is a specific example of claimed immunogenic
CC peptides having a sequence from hPTH(1-37) which includes the N- or C-
CC terminal alpha-helical region and/or the non-structured region of the
CC hormone. Antibodies and their binding fragments generated by injecting an
CC animal with the peptides are useful as diagnostic reagents for
CC determination of biologically active hPTH(1-37)
XX
SQ Sequence 9 AA;

Query Match 72.9%; Score 43; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMH 9
|||||||||
Db 1 SVSEIQLMH 9

RESULT 10
AAY96981
ID AAY96981 standard; peptide; 9 AA.
XX
AC AAY96981;
XX
DT 31-OCT-2000 (first entry)
XX
DE Parathyroid hormone N-terminal signaling domain.
XX
KW PTH; parathyroid hormone; N-terminal; signaling domain; bone mass;
KW bone reformation; resorption; remodeling; tether1; osteoporosis.
XX
OS Homo sapiens.
XX
PN WO200039278-A2.
XX
PD 06-JUL-2000.
XX
PF 30-DEC-1999; 99WO-US031108.
XX
PR 31-DEC-1998; 98US-0114577P.
XX
PA (GARD/) GARDELLA T J.
PA (KRON/) KRONENBERG H M.
PA (POTT/) POTTS J T.
PA (JUEP/) JUEPPNER H.
XX
PI Gardella TJ, Kronenberg HM, Potts JT, Jueppner H;
XX
DR WPI; 2000-452384/39.
XX
PT New compound comprising an amino terminal signaling functional domain
PT linked to a carboxy-terminal binding portion of parathyroid hormone for
PT treating mammalian conditions characterized by decreases in bone mass.
XX
PS Claim 11; Page 93; 119pp; English.
XX
CC Compounds of the structure or formula S-(L)_n-B, R_1-S-(L)_n-R or S-(L)_n
CC -R, are new. S is an amino terminal signaling functional domain of
CC parathyroid hormone (PTH); L is a linker molecule present n times (where
CC n is a positive integer 1-10 (preferably 4)); B is a C-terminal binding
CC portion of PTH(1-34) or a PTH-related protein (PTH-rP) (1-34); R_1 is the
CC PTH-1 receptor signal sequence; and R is (a portion of) PTH-1 receptor
CC sequence. The new compounds are used for treating mammalian conditions
CC characterized by decreases in bone mass, determining rates of bone
CC reformation, bone resorption and/or bone remodeling, treating diseases
CC and disorders associated with decreased tether1 activity, increasing cAMP
CC in a mammalian cell having PTH-1 receptors, or screening for a peptide or

```
CC   non-peptide PTH (claimed). The new compound can be administered by
CC   inhalation unlike the large native PTH or PTHrP which avoids the need for
CC   regular injections to treat osteoporosis
XX
SQ   Sequence 9 AA;

  Query Match             72.9%;  Score 43;  DB 3;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+06;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SVSEIQLMH 9
              |||||||||
Db          1 SVSEIQLMH 9


RESULT 11
AAB86220
ID   AAB86220 standard; peptide; 9 AA.
XX
AC   AAB86220;
XX
DT   03-SEP-2001  (first entry)
XX
DE   Human parathyroid hormone immunogenic peptide SEQ ID 2.
XX
KW   Parathyroid hormone; hPTH; immunogenic peptide; human; epitope;
KW   diagnosis; calcium-metabolism disorder; osteopathy; antagonist;
KW   hypo-parathyroidism; hyper-parathyroidism.
XX
OS   Homo sapiens.
XX
PN   DE19961350-A1.
XX
PD   21-JUN-2001.
XX
PF   17-DEC-1999;   99DE-01061350.
XX
PR   17-DEC-1999;   99DE-01061350.
XX
PA   (IMMU-) IMMUNDIAGNOSTIK AG.
XX
PI   Armbruster FP;
XX
DR   WPI; 2001-376318/40.
XX
PT   Determining the content of physiologically active parathyroid hormone,
PT   useful in diagnosis of calcium-metabolism disorders, using two antibodies
PT   reactive with different epitopes.
XX
PS   Disclosure; Page 3; 10pp; German.
XX
CC   This invention describes a novel method for determining (M1) the content
CC   of active parathyroid hormone (A) by treating a sample with (i) antibody
CC   (Ab1) that recognizes the epitope formed by amino acids (aa) 1-3 of (A),
CC   and including the N-terminal residue and (ii) antibody (Ab2) that
CC   recognizes an epitope within the receptor-binding site of (A). The number
CC   of molecules that react with both antibodies is determined and used to
CC   calculate the content of physiologically active (A). The method is used
CC   for diagnosis of calcium-metabolism disorders, osteopathy, or hypo- or
CC   hyper-parathyroidism. The method (unlike known assays) recognizes that
CC   (i) some fragments of (A) shorter than the complete (84 aa) peptide are
CC   active and (ii) that apparently intact peptide may be biologically
CC   inactive, and also takes into account the fact that some fragments of (A)
CC   are antagonistic (these have the receptor-binding site but lack the N-
CC   terminus). It thus provides a true measure of the content of
CC   physiologically active (A); contrast methods that measure intact peptide
CC   and its 1-37 fragment which may produce falsely high values. This
CC   sequence represents a peptide fragment used to illustrate the method of
CC   the invention
XX
SQ   Sequence 9 AA;

  Query Match             72.9%;  Score 43;  DB 4;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+06;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SVSEIQLMH 9
              |||||||||
Db          1 SVSEIQLMH 9


RESULT 12
AAY50600
ID   AAY50600 standard; peptide; 11 AA.
XX
AC   AAY50600;
XX
DT   09-FEB-2000  (first entry)
XX
DE   Resin bound cyclic peptide 33.
XX
KW   Cyclic peptide; resin bound; parathyroid hormone; osteopathic; disease;
KW   hypotensive; PTH receptor; treatment; hyper-calcemia; hypo-calcemia;
KW   osteoporosis; osteopenia; hyper-parathyroidism; hypo-parathyroidism;
KW   Cushing's syndrome; renal failure; hypertension; bone fracture repair.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 1
FT                   /note= "FMOC-Ala"
FT   Misc-difference 3
FT                   /note= "Ser(OtBu)"
FT   Misc-difference 4
FT                   /note= "Glu(OtBu)"
FT   Misc-difference 6
FT                   /note= "Gln(Trt)"
FT   Misc-difference 9
FT                   /note= "His(Trt)"
FT   Misc-difference 10
FT                   /note= "Asn(Trt)"
XX
PN   WO9952933-A1.
XX
PD   21-OCT-1999.
XX
PF   15-APR-1999;   99WO-US008435.
XX
PR   15-APR-1998;   98US-0081897P.
XX
PA   (RHON ) RHONE-POULENC RORER PHARM INC.
XX
PI   Sledeski AW,  Mencel JJ;
XX
DR   WPI; 1999-633822/54.
XX
PT   Convergent synthesis of peptides for treating e.g. bone disorders.
XX
PS   Disclosure; Page 75; 85pp; English.
XX
CC   This invention describes a novel method for the preparation of peptides
CC   (II) that contain both cyclic and linear peptide fragments comprises
CC   sequential reaction of a resin-bound linear fragment with the cyclic
CC   fragment in N-protected form and optionally other linear fragments. The
CC   products of the invention have osteopathic and hypotensive activity. (II)
CC   bind to hPTH receptors and act as agonists or antagonists of hPTH. The
CC   method is particularly used to prepare cyclic peptide analogs of
CC   parathyroid hormone (PTH) or PTH-related peptides which are useful for
CC   treating diseases that respond to treatment with agents that bind to PTH
CC   receptors (with or without activation of adenylyl cyclase activity), e.g.
CC   hyper- or hypo-calcemia, osteoporosis, osteopenia, hyper- or hypo-
CC   parathyroidism, Cushing's syndrome, renal failure and hypertension, also
CC   for promoting repair of bone fractures. Separate synthesis of the cyclic
CC   fragment allows convergent synthesis of resin-bound (II), with better
CC   yields and higher throughput. The difficulties associated with
CC   preparation of the bridged fragment are confined to a small peptide which
```

CC can be purified before reaction with the resin-bound component. AAY50568-
CC Y50614 represent the peptide fragments described in the method of the
CC invention
XX
SQ Sequence 11 AA;

Query Match 68.6%; Score 40.5; DB 2; Length 11;
Best Local Similarity 83.3%; Pred. No. 0.73;
Matches 10; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

Qy 1 SVSEIQLMHNLG 12
:|||||| ||||
Db 1 AVSEIQL-HNLG 11

RESULT 13
AAB01862
ID AAB01862 standard; peptide; 9 AA.
XX
AC AAB01862;
XX
DT 11-SEP-2000 (first entry)
XX
DE PTH(1-14)/PTHrP(1-14)-derived peptide, SEQ ID NO:6.
XX
KW Parathyroid hormone peptide; PTH; PTH-related peptide; PTHrP;
KW calcium homeostasis; PTH-1 receptor; PTH-2; vitamin D synthesis;
KW bone synthesis; agonist; osteoporosis; non-parenteral delivery.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200023594-A1.
XX
PD 27-APR-2000.
XX
PF 20-OCT-1999; 99WO-US024481.
XX
PR 22-OCT-1998; 98US-0105530P.
XX
PA (GARD/) GARDELLA T J.
PA (KRON/) KRONENBERG H M.
PA (POTT/) POTTS J T.
PA (JUEP/) JUEPPNER H.
XX
PI Gardella TJ, Kronenberg HM, Potts JT, Jueppner H;
XX
DR WPI; 2000-339693/29.
XX
PT Parathyroid hormone (PTH) peptides, PTH related peptides and the nucleic
PT acids that encode them, useful for treating osteoporosis.
XX
PS Disclosure; Page 26; 73pp; English.
XX
CC The invention relates to a novel parathyroid hormone (PTH) peptide
CC (AAB01859) and parathyroid hormone-related peptide (PTHrP; AAB01860), and
CC biologically active derivatives thereof (AAB01857-B01858, AAB01861-
CC B01869). The peptides of the invention are at least 85% identical to the
CC generic peptide of the formula: X1-Val-Ser-Glu-X2-Gln-Leu-X3-His-X4-X5-
CC Gly-Lys-X6 (AAB01857) where: X1 is Ser or Ala; X2 is Ile or Lys; X3 is
CC Met, Leu or Nle; X4 is Asn or Asp; X5 is Leu or Lys; X6 is His or Ser;
CC provided that the peptide is not PTHrP(1-14). The peptides of the
CC invention also encompass fragments of peptides of the invention
CC consisting of amino acids 1-9, 1-10, 1-11, 1-12 and 1-13, and N- and C-
CC terminal derivatives. PTH is a major regulator of calcium homeostasis,
CC and is necessary for the normal function of the gastrointestinal,
CC skeletal, neurological system, neuromuscular and cardiovascular systems.
CC It binds to both PTH-1 receptors on osteoblasts and renal tubular cells,
CC and to the recently identified PTH-2 receptor. PTH has a potent anabolic
CC effect on the skeleton, and mediates calcium reabsorption, enhances
CC phosphate clearance and vitamin D synthesis in the kidney. A homologous
CC calls of protein hormones, the PTH-related proteins (PTHrP) mimic some of
CC the renal and skeletal actions of PTH, and also bind to the PTH-1
CC receptor. They do not bind to the PTH-2 receptor. The peptides of the
CC invention are either agonists of PTH-1 and PTH-2 receptors (AAB01858,
CC AAB01861-B01866) or are PTH-1/PTH-2 receptor antagonists (AAB01867-
CC B01869). PTH-1/PTH-2 receptor agonists are useful for the treatment of
CC conditions characterised by a decrease in bone mass, such as
CC osteoporosis. PTH-1/PTH-2 receptor antagonists are useful for treating
CC medical disorders that arise from excessive or altered action of the PTH-
CC 1/PTH-2 receptor. Detectably labelled peptides of the invention are also
CC useful in the determination of rates of bone formation, bone resorption
CC and/or bone remodelling in a patient. The peptides of the invention are
CC "minimised" versions of PTH or PTHrP which are inexpensive to prepare by
CC conventional synthetic chemistry, and can be delivered to a patient via
CC non-parenteral routes. Sequences AAB01858 and AAB01861-B01866 represent
CC PTH-1/PTH-2 receptor agonists
XX
SQ Sequence 9 AA;

Query Match 67.8%; Score 40; DB 3; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.4e+06;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMH 9
:|||||||
Db 1 AVSEIQLMH 9

RESULT 14
AAY96966
ID AAY96966 standard; peptide; 9 AA.
XX
AC AAY96966;
XX
DT 31-OCT-2000 (first entry)
XX
DE Parathyroid hormone N-terminal signaling domain (residues 1-9).
XX
KW PTH; parathyroid hormone; N-terminal; signaling domain; bone mass;
KW bone reformation; resorption; remodeling; tether1; osteoporosis.
XX
OS Homo sapiens.
XX
PN WO200039278-A2.
XX
PD 06-JUL-2000.
XX
PF 30-DEC-1999; 99WO-US031108.
XX
PR 31-DEC-1998; 98US-0114577P.
XX
PA (GARD/) GARDELLA T J.
PA (KRON/) KRONENBERG H M.
PA (POTT/) POTTS J T.
PA (JUEP/) JUEPPNER H.
XX
PI Gardella TJ, Kronenberg HM, Potts JT, Jueppner H;
XX
DR WPI; 2000-452384/39.
XX
PT New compound comprising an amino terminal signaling functional domain
PT linked to a carboxy-terminal binding portion of parathyroid hormone for
PT treating mammalian conditions characterized by decreases in bone mass.
XX
PS Claim 4; Page 92; 119pp; English.
XX
CC Compounds of the structure or formula S-(L)_n-B, R_1-S-(L)_n-R or S-(L)_n
CC -R, are new. S is an amino terminal signaling functional domain of
CC parathyroid hormone (PTH); L is a linker molecule present n times (where
CC n is a positive integer 1-10 (preferably 4)); B is a C-terminal binding
CC portion of PTH(1-34) or a PTH-related protein (PTH-rP) (1-34); R_1 is the
CC PTH-1 receptor signal sequence; and R is (a portion of) PTH-1 receptor
CC sequence. The new compounds are used for treating mammalian conditions
CC characterized by decreases in bone mass, determining rates of bone
CC reformation, bone resorption and/or bone remodeling, treating diseases

CC and disorders associated with decreased tetherl activity, increasing cAMP
CC in a mammalian cell having PTH-1 receptors, or screening for a peptide or
CC non-peptide PTH (claimed). The new compound can be administered by
CC inhalation unlike the large native PTH or PTHrP which avoids the need for
CC regular injections to treat osteoporosis
XX
SQ Sequence 9 AA;

Query Match 67.8%; Score 40; DB 3; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.4e+06;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMH 9
:|||||||
Db 1 AVSEIQLMH 9

RESULT 15
AAB01863
ID AAB01863 standard; peptide; 9 AA.
XX
AC AAB01863;
XX
DT 11-SEP-2000 (first entry)
XX
DE PTH(1-14)/PTHrP(1-14)-derived peptide, SEQ ID NO:7.
XX
KW Parathyroid hormone peptide; PTH; PTH-related peptide; PTHrP;
KW calcium homeostasis; PTH-1 receptor; PTH-2; vitamin D synthesis;
KW bone synthesis; agonist; osteoporosis; non-parenteral delivery.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200023594-A1.
XX
PD 27-APR-2000.
XX
PF 20-OCT-1999; 99WO-US024481.
XX
PR 22-OCT-1998; 98US-0105530P.
XX
PA (GARD/) GARDELLA T J.
PA (KRON/) KRONENBERG H M.
PA (POTT/) POTTS J T.
PA (JUEP/) JUEPPNER H.
XX
PI Gardella TJ, Kronenberg HM, Potts JT, Jueppner H;
XX
DR WPI; 2000-339693/29.
XX
PT Parathyroid hormone (PTH) peptides, PTH related peptides and the nucleic
PT acids that encode them, useful for treating osteoporosis.
XX
PS Disclosure; Page 26; 73pp; English.
XX
CC The invention relates to a novel parathyroid hormone (PTH) peptide
CC (AAB01859) and parathyroid hormone-related peptide (PTHrP; AAB01860), and
CC biologically active derivatives thereof (AAB01857-B01858, AAB01861-
CC B01869). The peptides of the invention are at least 85% identical to the
CC generic peptide of the formula: X1-Val-Ser-Glu-X2-Gln-Leu-X3-His-X4-X5-
CC Gly-Lys-X6 (AAB01857) where: X1 is Ser or Ala; X2 is Ile or Lys; X3 is
CC Met, Leu or Nle; X4 is Asn or Asp; X5 is Leu or Lys; X6 is His or Ser;
CC provided that the peptide is not PTHrP(1-14). The peptides of the
CC invention also encompass fragments of peptides of the invention
CC consisting of amino acids 1-9, 1-10, 1-11, 1-12 and 1-13, and N- and C-
CC terminal derivatives. PTH is a major regulator of calcium homeostasis,
CC and is necessary for the normal function of the gastrointestinal,
CC skeletal, neurological system, neuromuscular and cardiovascular systems.
CC It binds to both PTH-1 receptors on osteoblasts and renal tubular cells,
CC and to the recently identified PTH-2 receptor. PTH has a potent anabolic
CC effect on the skeleton, and mediates calcium reabsorption, enhances
CC phosphate clearance and vitamin D synthesis in the kidney. A homologous
CC calls of protein hormones, the PTH-related proteins (PTHrP) mimic some of
CC the renal and skeletal actions of PTH, and also bind to the PTH-1
CC receptor. They do not bind to the PTH-2 receptor. The peptides of the
CC invention are either agonists of PTH-1 and PTH-2 receptors (AAB01858,
CC AAB01861-B01866) or are PTH-1/PTH-2 receptor antagonists (AAB01867-
CC B01869). PTH-1/PTH-2 receptor agonists are useful for the treatment of
CC conditions characterised by a decrease in bone mass, such as
CC osteoporosis. PTH-1/PTH-2 receptor antagonists are useful for treating
CC medical disorders that arise from excessive or altered action of the PTH-
CC 1/PTH-2 receptor. Detectably labelled peptides of the invention are also
CC useful in the determination of rates of bone formation, bone resorption
CC and/or bone remodelling in a patient. The peptides of the invention are
CC "minimised" versions of PTH or PTHrP which are inexpensive to prepare by
CC conventional synthetic chemistry, and can be delivered to a patient via
CC non-parenteral routes. Sequences AAB01858 and AAB01861-B01866 represent
CC PTH-1/PTH-2 receptor agonists
XX
SQ Sequence 9 AA;

Query Match 62.7%; Score 37; DB 3; Length 9;
Best Local Similarity 77.8%; Pred. No. 1.4e+06;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMH 9
:||||||:|
Db 1 AVSEIQLLH 9

Search completed: September 5, 2004, 09:34:30
Job time : 38.5 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: September 5, 2004, 09:37:09 ; Search time 32.5 Seconds
(without alignments)
116.332 Million cell updates/sec

Title: US-09-730-174A-3
Perfect score: 59
Sequence: 1 SVSEIQLMHNLG 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1298764 seqs, 315065143 residues

Total number of hits satisfying chosen parameters: 182187

Minimum DB seq length: 0
Maximum DB seq length: 12

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	59	100.0	12	9	US-09-730-174A-3	Sequence 3, Appli
2	56	94.9	12	9	US-09-730-174A-5	Sequence 5, Appli
3	55	93.2	11	9	US-09-730-174A-1	Sequence 1, Appli
4	55	93.2	12	9	US-09-730-174A-4	Sequence 4, Appli
5	52	88.1	12	9	US-09-730-174A-6	Sequence 6, Appli
6	51	86.4	11	9	US-09-730-174A-2	Sequence 2, Appli
7	49	83.1	10	14	US-10-168-185-1	Sequence 1, Appli
8	45	76.3	9	14	US-10-168-185-7	Sequence 7, Appli
9	43	72.9	9	14	US-10-168-185-2	Sequence 2, Appli
10	41	69.5	8	14	US-10-168-185-8	Sequence 8, Appli
11	40	67.8	9	14	US-10-192-673-6	Sequence 6, Appli
12	37	62.7	9	14	US-10-192-673-7	Sequence 7, Appli
13	35	59.3	8	14	US-10-168-185-3	Sequence 3, Appli
14	33	55.9	9	14	US-10-192-673-10	Sequence 10, Appl
15	30	50.8	7	14	US-10-168-185-4	Sequence 4, Appli
16	30	50.8	9	14	US-10-192-673-8	Sequence 8, Appli
17	29	49.2	10	14	US-10-033-741-61	Sequence 61, Appl
18	28	47.5	9	9	US-09-746-945-6	Sequence 6, Appli
19	28	47.5	12	14	US-10-319-130-16	Sequence 16, Appl
20	27	45.8	11	16	US-10-391-364-93	Sequence 93, Appl
21	26	44.1	6	14	US-10-168-185-5	Sequence 5, Appli
22	26	44.1	10	14	US-10-168-185-11	Sequence 11, Appl
23	25	42.4	11	12	US-09-747-287-185	Sequence 185, App
24	25	42.4	11	12	US-09-874-350A-151	Sequence 151, App
25	24	40.7	10	9	US-09-826-290-27	Sequence 27, Appl
26	24	40.7	10	16	US-10-264-309-369	Sequence 369, App
27	24	40.7	10	16	US-10-432-234A-75	Sequence 75, Appl
28	24	40.7	10	16	US-10-432-234A-76	Sequence 76, Appl
29	24	40.7	10	16	US-10-432-234A-77	Sequence 77, Appl
30	24	40.7	11	12	US-10-609-217-41	Sequence 41, Appl
31	24	40.7	11	12	US-10-632-388-41	Sequence 41, Appl
32	24	40.7	11	12	US-10-651-723-41	Sequence 41, Appl
33	24	40.7	11	12	US-10-645-761-41	Sequence 41, Appl
34	24	40.7	11	16	US-10-666-696-41	Sequence 41, Appl
35	24	40.7	11	16	US-10-653-048-41	Sequence 41, Appl
36	24	40.7	12	14	US-10-286-457-294	Sequence 294, App
37	23	39.0	7	14	US-10-286-457-469	Sequence 469, App
38	23	39.0	7	15	US-10-368-280-12	Sequence 12, Appl
39	23	39.0	7	15	US-10-374-035-12	Sequence 12, Appl
40	23	39.0	9	9	US-09-894-018-332	Sequence 332, App
41	23	39.0	9	10	US-09-821-734-4	Sequence 4, Appli
42	23	39.0	9	10	US-09-854-248-11	Sequence 11, Appl
43	23	39.0	9	12	US-10-253-286-288	Sequence 288, App
44	23	39.0	9	14	US-10-094-699-50	Sequence 50, Appl
45	23	39.0	9	15	US-10-117-937-249	Sequence 249, App

ALIGNMENTS

RESULT 1
US-09-730-174A-3
; Sequence 3, Application US/09730174A
; Patent No. US20020110871A1
; GENERAL INFORMATION:
; APPLICANT: Zahradnik, R.J.
; TITLE OF INVENTION: Antibodies and Peptide Antigens for Producing Antibodies having a
; TITLE OF INVENTION: Selective Binding Specificity to Bioactive Intact Parathyroid Ho
; FILE REFERENCE: IMUNE-001A
; CURRENT APPLICATION NUMBER: US/09/730,174A
; CURRENT FILING DATE: 2000-12-05
; NUMBER OF SEQ ID NOS: 12
; SEQ ID NO 3
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Induces Formation of Antibodies and Isolates said Antibodies
US-09-730-174A-3

Query Match 100.0%; Score 59; DB 9; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.00081;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLG 12
||||||||||||
Db 1 SVSEIQLMHNLG 12

RESULT 2
US-09-730-174A-5
; Sequence 5, Application US/09730174A
; Patent No. US20020110871A1
; GENERAL INFORMATION:
; APPLICANT: Zahradnik, R.J.
; TITLE OF INVENTION: Antibodies and Peptide Antigens for Producing Antibodies having a
; TITLE OF INVENTION: Selective Binding Specificity to Bioactive Intact Parathyroid Ho
; FILE REFERENCE: IMUNE-001A

```
;  CURRENT APPLICATION NUMBER: US/09/730,174A
;  CURRENT FILING DATE:  2000-12-05
;  NUMBER OF SEQ ID NOS: 12
; SEQ ID NO 5
;   LENGTH: 12
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Induces Formation of Antibodies and Isolates said Antibodies
US-09-730-174A-5

  Query Match             94.9%;  Score 56;  DB 9;  Length 12;
  Best Local Similarity   91.7%;  Pred. No. 0.0027;
  Matches   11;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SVSEIQLMHNLG 12
              :||||||||||||
Db          1 AVSEIQLMHNLG 12


RESULT 3
US-09-730-174A-1
; Sequence 1, Application US/09730174A
; Patent No. US20020110871A1
; GENERAL INFORMATION:
;  APPLICANT: Zahradnik, R.J.
;  TITLE OF INVENTION: Antibodies and Peptide Antigens for Producing Antibodies having a
;  TITLE OF INVENTION:  Selective Binding Specificity to Bioactive Intact Parathyroid Ho
;  FILE REFERENCE: IMUNE-001A
;  CURRENT APPLICATION NUMBER: US/09/730,174A
;  CURRENT FILING DATE:  2000-12-05
;  NUMBER OF SEQ ID NOS: 12
; SEQ ID NO 1
;   LENGTH: 11
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Induces Formation of Antibodies and Isolates said Antibodies
US-09-730-174A-1

  Query Match             93.2%;  Score 55;  DB 9;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 0.0038;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 VSEIQLMHNLG 12
              ||||||||||||
Db          1 VSEIQLMHNLG 11


RESULT 4
US-09-730-174A-4
; Sequence 4, Application US/09730174A
; Patent No. US20020110871A1
; GENERAL INFORMATION:
;  APPLICANT: Zahradnik, R.J.
;  TITLE OF INVENTION: Antibodies and Peptide Antigens for Producing Antibodies having a
;  TITLE OF INVENTION:  Selective Binding Specificity to Bioactive Intact Parathyroid Ho
;  FILE REFERENCE: IMUNE-001A
;  CURRENT APPLICATION NUMBER: US/09/730,174A
;  CURRENT FILING DATE:  2000-12-05
;  NUMBER OF SEQ ID NOS: 12
; SEQ ID NO 4
;   LENGTH: 12
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Induces Formation of Antibodies and Isolates said Antibodies
US-09-730-174A-4

  Query Match             93.2%;  Score 55;  DB 9;  Length 12;
  Best Local Similarity   91.7%;  Pred. No. 0.0041;
  Matches   11;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 SVSEIQLMHNLG 12
              ||||||.|||||
Db          1 SVSEIQFMHNLG 12


RESULT 5
US-09-730-174A-6
; Sequence 6, Application US/09730174A
; Patent No. US20020110871A1
; GENERAL INFORMATION:
;  APPLICANT: Zahradnik, R.J.
;  TITLE OF INVENTION: Antibodies and Peptide Antigens for Producing Antibodies having a
;  TITLE OF INVENTION:  Selective Binding Specificity to Bioactive Intact Parathyroid Ho
;  FILE REFERENCE: IMUNE-001A
;  CURRENT APPLICATION NUMBER: US/09/730,174A
;  CURRENT FILING DATE:  2000-12-05
;  NUMBER OF SEQ ID NOS: 12
; SEQ ID NO 6
;   LENGTH: 12
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Induces Formation of Antibodies and Isolates said Antibodies
US-09-730-174A-6

  Query Match             88.1%;  Score 52;  DB 9;  Length 12;
  Best Local Similarity   83.3%;  Pred. No. 0.014;
  Matches   10;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 SVSEIQLMHNLG 12
              :|||||.|||||
Db          1 AVSEIQFMHNLG 12


RESULT 6
US-09-730-174A-2
; Sequence 2, Application US/09730174A
; Patent No. US20020110871A1
; GENERAL INFORMATION:
;  APPLICANT: Zahradnik, R.J.
;  TITLE OF INVENTION: Antibodies and Peptide Antigens for Producing Antibodies having a
;  TITLE OF INVENTION:  Selective Binding Specificity to Bioactive Intact Parathyroid Ho
;  FILE REFERENCE: IMUNE-001A
;  CURRENT APPLICATION NUMBER: US/09/730,174A
;  CURRENT FILING DATE:  2000-12-05
;  NUMBER OF SEQ ID NOS: 12
; SEQ ID NO 2
;   LENGTH: 11
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Induces Formation of Antibodies and Isolates said Antibodies
US-09-730-174A-2

  Query Match             86.4%;  Score 51;  DB 9;  Length 11;
  Best Local Similarity   90.9%;  Pred. No. 0.019;
  Matches   10;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 VSEIQLMHNLG 12
              |||||.|||||
Db          1 VSEIQFMHNLG 11


RESULT 7
US-10-168-185-1
; Sequence 1, Application US/10168185
; Publication No. US20030175802A1
; GENERAL INFORMATION:
;  APPLICANT: Armbruster, Franz Paul
;  APPLICANT:  Missbichler, Albert
;  APPLICANT:  Schmidt-Gayk, Heinrich
;  APPLICANT:  Roth, Heinz-Jurgen
;  TITLE OF INVENTION: Method for Determining Parathormone
```

```
;  TITLE OF INVENTION:  Activity in a Human Sample
;  FILE REFERENCE: HLZ-004US
;  CURRENT APPLICATION NUMBER: US/10/168,185
;  CURRENT FILING DATE:  2002-06-17
;  PRIOR APPLICATION NUMBER: PCT/EP00/12911
;  PRIOR FILING DATE: 2000-12-18
;  PRIOR APPLICATION NUMBER: DE 19961350
;  PRIOR FILING DATE: 1999-12-17
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 10
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-168-185-1

  Query Match             83.1%;  Score 49;  DB 14;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 0.04;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SVSEIQLMHN 10
              ||||||||||
Db          1 SVSEIQLMHN 10


RESULT 8
US-10-168-185-7
; Sequence 7, Application US/10168185
; Publication No. US20030175802A1
; GENERAL INFORMATION:
;  APPLICANT: Armbruster, Franz Paul
;  APPLICANT:  Missbichler, Albert
;  APPLICANT:  Schmidt-Gayk, Heinrich
;  APPLICANT:  Roth, Heinz-Jurgen
;  TITLE OF INVENTION: Method for Determining Parathormone
;  TITLE OF INVENTION:  Activity in a Human Sample
;  FILE REFERENCE: HLZ-004US
;  CURRENT APPLICATION NUMBER: US/10/168,185
;  CURRENT FILING DATE:  2002-06-17
;  PRIOR APPLICATION NUMBER: PCT/EP00/12911
;  PRIOR FILING DATE: 2000-12-18
;  PRIOR APPLICATION NUMBER: DE 19961350
;  PRIOR FILING DATE: 1999-12-17
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-168-185-7

  Query Match             76.3%;  Score 45;  DB 14;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+06;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 VSEIQLMHN 10
              |||||||||
Db          1 VSEIQLMHN 9


RESULT 9
US-10-168-185-2
; Sequence 2, Application US/10168185
; Publication No. US20030175802A1
; GENERAL INFORMATION:
;  APPLICANT: Armbruster, Franz Paul
;  APPLICANT:  Missbichler, Albert
;  APPLICANT:  Schmidt-Gayk, Heinrich
;  APPLICANT:  Roth, Heinz-Jurgen
;  TITLE OF INVENTION: Method for Determining Parathormone
;  TITLE OF INVENTION:  Activity in a Human Sample
;  FILE REFERENCE: HLZ-004US
;  CURRENT APPLICATION NUMBER: US/10/168,185
;  CURRENT FILING DATE:  2002-06-17
;  PRIOR APPLICATION NUMBER: PCT/EP00/12911
;  PRIOR FILING DATE: 2000-12-18
;  PRIOR APPLICATION NUMBER: DE 19961350
;  PRIOR FILING DATE: 1999-12-17
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-168-185-2

  Query Match             72.9%;  Score 43;  DB 14;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+06;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SVSEIQLMH 9
              |||||||||
Db          1 SVSEIQLMH 9


RESULT 10
US-10-168-185-8
; Sequence 8, Application US/10168185
; Publication No. US20030175802A1
; GENERAL INFORMATION:
;  APPLICANT: Armbruster, Franz Paul
;  APPLICANT:  Missbichler, Albert
;  APPLICANT:  Schmidt-Gayk, Heinrich
;  APPLICANT:  Roth, Heinz-Jurgen
;  TITLE OF INVENTION: Method for Determining Parathormone
;  TITLE OF INVENTION:  Activity in a Human Sample
;  FILE REFERENCE: HLZ-004US
;  CURRENT APPLICATION NUMBER: US/10/168,185
;  CURRENT FILING DATE:  2002-06-17
;  PRIOR APPLICATION NUMBER: PCT/EP00/12911
;  PRIOR FILING DATE: 2000-12-18
;  PRIOR APPLICATION NUMBER: DE 19961350
;  PRIOR FILING DATE: 1999-12-17
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
;   LENGTH: 8
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-168-185-8

  Query Match             69.5%;  Score 41;  DB 14;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+06;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 SEIQLMHN 10
              ||||||||
Db          1 SEIQLMHN 8


RESULT 11
US-10-192-673-6
; Sequence 6, Application US/10192673
; Publication No. US20030166838A1
; GENERAL INFORMATION:
;  APPLICANT: Gardella, Thomas J.
;  APPLICANT:  Kronenberg, Henry
;  APPLICANT:  Potts, John T.
;  APPLICANT:  Juppner, Harald
;  TITLE OF INVENTION: Bioactive Peptides and Peptide Derivatives of
;  TITLE OF INVENTION:  Parathyroid Hormone (PTH) and Parathyroid
;  TITLE OF INVENTION:  Hormone-Related Peptide (PTHrP)
;  FILE REFERENCE: 0609.4570002
;  CURRENT APPLICATION NUMBER: US/10/192,673
;  CURRENT FILING DATE:  2002-07-11
;  PRIOR APPLICATION NUMBER: U.S. 09/421,379
```

```
;  PRIOR FILING DATE: 1999-10-20
;  PRIOR APPLICATION NUMBER: U.S. 60/105,530
;  PRIOR FILING DATE: 1998-10-22
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: synthetic
;   OTHER INFORMATION: peptide
US-10-192-673-6

  Query Match             67.8%;  Score 40;  DB 14;  Length 9;
  Best Local Similarity   88.9%;  Pred. No. 1.2e+06;
  Matches    8;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SVSEIQLMH 9
              :||||||||
Db          1 AVSEIQLMH 9


RESULT 12
US-10-192-673-7
; Sequence 7, Application US/10192673
; Publication No. US20030166838A1
; GENERAL INFORMATION:
;  APPLICANT: Gardella, Thomas J.
;  APPLICANT:  Kronenberg, Henry
;  APPLICANT:  Potts, John T.
;  APPLICANT:  Juppner, Harald
;  TITLE OF INVENTION: Bioactive Peptides and Peptide Derivatives of
;  TITLE OF INVENTION:  Parathyroid Hormone (PTH) and Parathyroid
;  TITLE OF INVENTION:  Hormone-Related Peptide (PTHrP)
;  FILE REFERENCE: 0609.4570002
;  CURRENT APPLICATION NUMBER: US/10/192,673
;  CURRENT FILING DATE:  2002-07-11
;  PRIOR APPLICATION NUMBER: U.S. 09/421,379
;  PRIOR FILING DATE: 1999-10-20
;  PRIOR APPLICATION NUMBER: U.S. 60/105,530
;  PRIOR FILING DATE: 1998-10-22
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: synthetic
;   OTHER INFORMATION: peptide
US-10-192-673-7

  Query Match             62.7%;  Score 37;  DB 14;  Length 9;
  Best Local Similarity   77.8%;  Pred. No. 1.2e+06;
  Matches    7;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SVSEIQLMH 9
              :||||||:|
Db          1 AVSEIQLLH 9


RESULT 13
US-10-168-185-3
; Sequence 3, Application US/10168185
; Publication No. US20030175802A1
; GENERAL INFORMATION:
;  APPLICANT: Armbruster, Franz Paul
;  APPLICANT:  Missbichler, Albert
;  APPLICANT:  Schmidt-Gayk, Heinrich
;  APPLICANT:  Roth, Heinz-Jurgen
;  TITLE OF INVENTION: Method for Determining Parathormone
;  TITLE OF INVENTION:  Activity in a Human Sample
;  FILE REFERENCE: HLZ-004US
;  CURRENT APPLICATION NUMBER: US/10/168,185
;  CURRENT FILING DATE:  2002-06-17
;  PRIOR APPLICATION NUMBER: PCT/EP00/12911
;  PRIOR FILING DATE: 2000-12-18
;  PRIOR APPLICATION NUMBER: DE 19961350
;  PRIOR FILING DATE: 1999-12-17
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;   LENGTH: 8
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-168-185-3

  Query Match             59.3%;  Score 35;  DB 14;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+06;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SVSEIQLM 8
              ||||||||
Db          1 SVSEIQLM 8


RESULT 14
US-10-192-673-10
; Sequence 10, Application US/10192673
; Publication No. US20030166838A1
; GENERAL INFORMATION:
;  APPLICANT: Gardella, Thomas J.
;  APPLICANT:  Kronenberg, Henry
;  APPLICANT:  Potts, John T.
;  APPLICANT:  Juppner, Harald
;  TITLE OF INVENTION: Bioactive Peptides and Peptide Derivatives of
;  TITLE OF INVENTION:  Parathyroid Hormone (PTH) and Parathyroid
;  TITLE OF INVENTION:  Hormone-Related Peptide (PTHrP)
;  FILE REFERENCE: 0609.4570002
;  CURRENT APPLICATION NUMBER: US/10/192,673
;  CURRENT FILING DATE:  2002-07-11
;  PRIOR APPLICATION NUMBER: U.S. 09/421,379
;  PRIOR FILING DATE: 1999-10-20
;  PRIOR APPLICATION NUMBER: U.S. 60/105,530
;  PRIOR FILING DATE: 1998-10-22
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: synthetic
;   OTHER INFORMATION: peptide
US-10-192-673-10

  Query Match             55.9%;  Score 33;  DB 14;  Length 9;
  Best Local Similarity   77.8%;  Pred. No. 1.2e+06;
  Matches    7;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 SVSEIQLMH 9
              |||| ||:|
Db          1 SVSEHQLLH 9


RESULT 15
US-10-168-185-4
; Sequence 4, Application US/10168185
; Publication No. US20030175802A1
; GENERAL INFORMATION:
;  APPLICANT: Armbruster, Franz Paul
;  APPLICANT:  Missbichler, Albert
;  APPLICANT:  Schmidt-Gayk, Heinrich
;  APPLICANT:  Roth, Heinz-Jurgen
;  TITLE OF INVENTION: Method for Determining Parathormone
```

```
;  TITLE OF INVENTION:  Activity in a Human Sample
;  FILE REFERENCE: HLZ-004US
;  CURRENT APPLICATION NUMBER: US/10/168,185
;  CURRENT FILING DATE:  2002-06-17
;  PRIOR APPLICATION NUMBER: PCT/EP00/12911
;  PRIOR FILING DATE: 2000-12-18
;  PRIOR APPLICATION NUMBER: DE 19961350
;  PRIOR FILING DATE: 1999-12-17
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
;   LENGTH: 7
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-168-185-4

  Query Match             50.8%;  Score 30;  DB 14;  Length 7;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+06;
  Matches    7;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SVSEIQL 7
              |||||||
Db          1 SVSEIQL 7


Search completed: September  5, 2004, 09:49:37
Job time : 33.5 secs
```

This Page Blank (uspto)

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: September 5, 2004, 09:30:43 ; Search time 9.5 Seconds
(without alignments)
121.505 Million cell updates/sec

Title: US-09-730-174A-4
Perfect score: 61
Sequence: 1 SVSEIQFMHNLG 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 1581

Minimum DB seq length: 0
Maximum DB seq length: 12

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	23	37.7	10	2	S28055	cytochrome b559 co
2	18	29.5	7	2	A58718	carnocin UI49 - Ca
3	18	29.5	9	2	S78420	ribosomal protein
4	18	29.5	10	2	A60589	sperm-activating p
5	17	27.9	8	2	A05169	neuropeptide M-I -
6	17	27.9	10	2	A37268	Ig heavy chain C r
7	17	27.9	12	2	S21205	Ig heavy chain V r
8	17	27.9	12	2	PH1187	T-cell receptor al
9	16	26.2	7	2	I46868	alpha-myosin heavy
10	16	26.2	9	2	G58502	kidney and bladder
11	16	26.2	10	2	JC1416	hypertrehalosemic
12	16	26.2	10	2	S09138	hypertrehalosemic
13	16	26.2	11	2	A32428	amine oxidase (cop
14	15	24.6	7	2	S29735	polyphosphate-gluc
15	15	24.6	9	2	PT0231	Ig heavy chain CDR
16	15	24.6	9	2	A56029	N-methylpurine DNA
17	15	24.6	10	2	S33844	alpha-2-macroglobu
18	15	24.6	10	2	S27873	hypothetical prote
19	15	24.6	10	2	S38304	lectin GNL1 alpha
20	15	24.6	11	2	A38841	rhodopsin homolog
21	15	24.6	11	2	S35490	type II site-speci
22	15	24.6	12	2	PH1190	T-cell receptor al
23	15	24.6	12	2	S51737	T-cell receptor be
24	14	23.0	4	2	A35779	neuropeptide Antho
25	14	23.0	7	2	JN0859	peptidyl-dipeptida
26	14	23.0	7	2	S78024	ribosomal protein
27	14	23.0	8	2	S08995	hypertrehalosemic
28	14	23.0	8	2	A49823	adipokinetic hormo
29	14	23.0	8	2	A44960	neuropeptide Led-C
30	14	23.0	9	2	PW0002	chlorophyll a/b-bi
31	14	23.0	9	2	S13636	coat protein beta
32	14	23.0	9	2	PT0238	Ig heavy chain CRD
33	14	23.0	10	1	SPPGNK	neuromedin K - pig
34	14	23.0	10	2	C61033	ranatachykinin C -
35	14	23.0	10	2	B46453	e antigen p20e pre
36	14	23.0	10	2	S70251	nitrogenase (EC 1.
37	14	23.0	11	2	B41835	translation elonga
38	14	23.0	11	2	S19301	endo-1,4-beta-xyla
39	14	23.0	11	2	PA0028	protein QA300042 -
40	14	23.0	11	2	S60354	retinal oxidase -
41	14	23.0	11	2	S53436	beta-D-galactosida
42	14	23.0	11	2	PH0904	T-cell receptor be
43	14	23.0	12	1	A43975	locustamyotropin -
44	14	23.0	12	2	S25485	transcription fact
45	14	23.0	12	2	S71034	potB protein - Sal

ALIGNMENTS

RESULT 1
S28055
cytochrome b559 component psbF - pepper chloroplast (fragment)
C;Species: chloroplast Capsicum annuum (pepper)
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 11-Jun-1999
C;Accession: S28055
R;Kuntz, M.; Camara, B.; Weil, J.H.; Schantz, R.
Plant Mol. Biol. 20, 1185-1188, 1992
A;Title: The psbL gene from bell pepper (Capsicum annuum): plastid RNA editing also occu
A;Reference number: S28055; MUID:93099270; PMID:1463853
A;Accession: S28055
A;Molecule type: DNA
A;Residues: 1-10 <KUN>
A;Cross-references: EMBL:X65570; NID:g14344; PIDN:CAA46539.1; PID:g415734
C;Genetics:
A;Gene: psbF
A;Genome: chloroplast
C;Superfamily: cytochrome b559 component F
C;Keywords: chloroplast; photosynthesis; photosystem II; thylakoid

Query Match 37.7%; Score 23; DB 2; Length 10;
Best Local Similarity 50.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 SVSEIQFM 8
              |:| :||:
Db          1 SISAMQFI 8
```

RESULT 2
A58718
carnocin UI49 - Carnobacterium sp. (fragment)
C;Species: Carnobacterium sp.
C;Date: 23-Jan-1998 #sequence_revision 30-Jan-1998 #text_change 30-Jan-1998
C;Accession: A58718
R;Stoffels, G.; Nissen-Meyer, J.; Gudmundsdottir, A.; Sletten, K.; Holo, H.; Nes, I.F.
Appl. Environ. Microbiol. 58, 1417-1422, 1992
A;Title: Purification and characterization of a new bacteriocin isolated from a Carnoba
A;Reference number: A58718; MUID:92321768; PMID:1622206
A;Accession: A58718
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-7 <STO>
C;Keywords: antibiotic; lanthionine

Query Match 29.5%; Score 18; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          3 SEIQ 6
              ||||
Db          2 SEIQ 5
```

RESULT 3
S78420
ribosomal protein RL41, mitochondrial [validated] - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 25-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 21-Jul-2000
C;Accession: S78420
R;Goldschmidt-Reisin, S.; Graack, H.R.
submitted to the Protein Sequence Database, February 1998
A;Reference number: S78411
A;Accession: S78420
A;Molecule type: protein
A;Residues: 1-9 <GOL>
A;Note: the protein is designated as mitochondrial ribosomal protein L41
C;Keywords: mitochondrion; protein biosynthesis; ribosome

Query Match 29.5%; Score 18; DB 2; Length 9;
Best Local Similarity 75.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 HNLG 12
| ||
Db 5 HRLG 8

RESULT 4
A60589
sperm-activating peptide (Tyr-2, Asn-3, Gly-5, Ile-9, Asp-10 SAP-I) - slate-pencil urchi
C;Species: Heterocentrotus mamillatus
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 18-Aug-2000
C;Accession: A60589
R;Yoshino, K.I.; Kajiura, H.; Nomura, K.; Takao, T.; Shimonishi, Y.; Kurita, M.; Yamaguc
Comp. Biochem. Physiol. B 94, 739-751, 1989
A;Title: A halogenated amino acid-containing sperm activating peptide and its related pe
otus nudus, Echinometra mathaei and Heterocentrotus mammillatus.
A;Reference number: A60527
A;Accession: A60589
A;Molecule type: protein
A;Residues: 1-10 <YOS>
C;Superfamily: unassigned animal peptides

Query Match 29.5%; Score 18; DB 2; Length 10;
Best Local Similarity 75.0%; Pred. No. 2e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 9 HNLG 12
:|||
Db 2 YNLG 5

RESULT 5
A05169
neuropeptide M-I - American cockroach
C;Species: Periplaneta americana (American cockroach)
C;Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 31-Dec-1993
C;Accession: A05169
R;Witten, J.L.; Schaffer, M.H.; O'Shea, M.; Cook, J.C.; Hemling, M.E.; Rinehart Jr., K.L
Biochem. Biophys. Res. Commun. 124, 350-358, 1984
A;Title: Structures of two cockroach neuropeptides assigned by fast atom bombardment mas
A;Reference number: A90118; MUID:85046530; PMID:6548628
A;Accession: A05169
A;Molecule type: protein
A;Residues: 1-8 <WIT>
C;Keywords: neuropeptide

Query Match 27.9%; Score 17; DB 2; Length 8;
Best Local Similarity 42.9%; Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 4 EIQFMHN 10
|: | |
Db 1 EVNFSPN 7

RESULT 6
A37268
Ig heavy chain C region (129) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 19-Mar-1997 #sequence_revision 13-Mar-1998 #text_change 13-Mar-1998
C;Accession: A37268
R;Ruff-Jamison, S.; Campos-Gonzalez, R.; Glenney Jr., J.R.
J. Biol. Chem. 266, 6607-6613, 1991
A;Title: Heavy and light chain variable region sequences and antibody properties of anti
A;Reference number: A38740; MUID:91177923; PMID:1706720
A;Accession: A37268
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-10 <RUF>

Query Match 27.9%; Score 17; DB 2; Length 10;
Best Local Similarity 44.4%; Pred. No. 3.1e+03;
Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 4 EIQFMHNLG 12
| | |:|
Db 1 ESQSFPNVG 9

RESULT 7
S21205
Ig heavy chain V region - human
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 16-Aug-1996
C;Accession: S21205
R;Makiya, R.; Stigbrand, T.
Eur. J. Biochem. 205, 341-345, 1992
A;Title: Placental alkaline phosphatase has a binding site for the human immunoglobulin-
A;Reference number: S21205; MUID:92209522; PMID:1555592
A;Accession: S21205
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-12 <MAK>
C;Keywords: heterotetramer; immunoglobulin

Query Match 27.9%; Score 17; DB 2; Length 12;
Best Local Similarity 33.3%; Pred. No. 3.8e+03;
Matches 3; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 4 EIQFMHNLG 12
|:| : : |
Db 1 EVQLVESGG 9

RESULT 8
PH1187
T-cell receptor alpha chain V region (Cw3/1F11) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
C;Accession: PH1187
R;Casanova, J.L.; Cerottini, J.C.; Matthes, M.; Necker, A.; Gournier, H.; Barra, C.; Wid
J. Exp. Med. 176, 439-447, 1992
A;Title: H-2-restricted cytolytic T lymphocytes specific for HLA display T cell receptor
A;Reference number: S26512; MUID:92364546; PMID:1380061
A;Accession: PH1187
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-12 <CAS>

Query Match 27.9%; Score 17; DB 2; Length 12;
Best Local Similarity 57.1%; Pred. No. 3.8e+03;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 SVSEIQF 7
:||| |
Db 2 AVSETGF 8

```
RESULT 9
I46868
alpha-myosin heavy chain - rabbit (fragment)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 14-Feb-1997 #sequence_revision 14-Feb-1997 #text_change 05-Nov-1999
C;Accession: I46868
R;Friedman, D.J.; Umeda, P.K.; Sinha, A.M.; Hsu, H.
Proc. Natl. Acad. Sci. U.S.A. 81, 3044-3048, 1984
A;Title: Characterization of genomic clones specifying rabbit alpha- and beta-ventricula
A;Reference number: I46868; MUID:84221901; PMID:6328491
A;Accession: I46868
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-7 <FRI>
A;Cross-references: GB:K01698; NID:g165538; PIDN:AAA31415.1; PID:g165539

  Query Match           26.2%;  Score 16;  DB 2;  Length 7;
  Best Local Similarity   60.0%;  Pred. No. 2.8e+05;
  Matches    3;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          6 QFMHN 10
              | ||:
Db          1 QKMHD 5


RESULT 10
G58502
kidney and bladder stone protein - unidentified bacterium (fragment)
C;Species: unidentified bacterium
C;Date: 07-Feb-1997 #sequence_revision 07-Feb-1997 #text_change 10-Jul-1998
C;Accession: G58502
R;Binette, J.P.; Binette, M.B.
submitted to the Protein Sequence Database, October 1996
A;Description: The proteins of kidney and gallbladder stones.
A;Reference number: A58501
A;Accession: G58502
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-9 <BIN>
A;Experimental source: human kidney stone, bladder stone
A;Note: a secondary sequence AAKENPXD was also found

  Query Match           26.2%;  Score 16;  DB 2;  Length 9;
  Best Local Similarity   28.6%;  Pred. No. 2.8e+05;
  Matches    2;  Conservative    4;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 SVSEIQF 7
              |: :::|
Db          1 SLPDVKF 7


RESULT 11
JC1416
hypertrehalosemic hormone I - stick insect (Carausius morosus)
N;Alternate names: neuropeptide Cam-HrTH-I
N;Contains: hypertrehalosemic factor II
C;Species: Carausius morosus
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C;Accession: JC1416; S07157
R;Gaede, G.; Kellner, R.; Rinehart, K.L.; Proefke, M.L.
Biochem. Biophys. Res. Commun. 189, 1303-1309, 1992
A;Title: A tryptophan-substituted member of the AKH/RPCH family isolated from a stick in
A;Reference number: JC1416; MUID:93129188; PMID:1482345
A;Accession: JC1416
A;Molecule type: protein
A;Residues: 1-10 <GAE1>
R;Gaede, G.; Rinehart Jr., K.L.
Biol. Chem. Hoppe-Seyler 368, 67-75, 1987
A;Title: Primary structure of the hypertrehalosaemic factor II from the corpus cardiacum
A;Reference number: S07157; MUID:87157103; PMID:3828078
A;Accession: S07157
A;Molecule type: protein
A;Residues: 'Z',2-10 <GAE2>
C;Comment: Hypertrehalosemic factor II lacks the tryptophan modification.
C;Comment: This peptide raises hemolymph levels of trehalose in the cockroach Periplanet
C;Superfamily: adipokinetic hormone
C;Keywords: amidated carboxyl end; glycoprotein; hormone; neuropeptide; pyroglutamic ac
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;8/Binding site: carbohydrate (Trp) (covalent) #status experimental
F;10/Modified site: amidated carboxyl end (Thr) #status experimental

  Query Match           26.2%;  Score 16;  DB 2;  Length 10;
  Best Local Similarity   33.3%;  Pred. No. 4.8e+03;
  Matches    3;  Conservative    2;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          4 EIQFMHNLG 12
              :: |  | |
Db          1 QLTFTPNWG 9


RESULT 12
S09138
hypertrehalosemic hormone II - stick insect (Extatosoma tiaratum)
N;Alternate names: Cam-HrTH-II
C;Species: Extatosoma tiaratum
C;Date: 30-Jun-1992 #sequence_revision 24-Oct-1997 #text_change 31-Oct-1997
C;Accession: S09138
R;Gaede, G.; Rinehart, K.L.
Biol. Chem. Hoppe-Seyler 371, 345-354, 1990
A;Title: Primary structures of hypertrehalosaemic neuropeptides isolated from the corpo
entalis and of the stick insect Extatosoma tiaratum assigned by tandem fast atom bombar
A;Reference number: S08995; MUID:90253659; PMID:2340112
A;Accession: S09138
A;Molecule type: protein
A;Residues: 1-10 <GAE>
A;Note: the amino-terminal residue forms pyrrolidone carboxylic acid; therefore, we hav
C;Superfamily: adipokinetic hormone
C;Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;10/Modified site: amidated carboxyl end (Thr) #status experimental

  Query Match           26.2%;  Score 16;  DB 2;  Length 10;
  Best Local Similarity   33.3%;  Pred. No. 4.8e+03;
  Matches    3;  Conservative    2;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          4 EIQFMHNLG 12
              :: |  | |
Db          1 QLTFTPNWG 9


RESULT 13
A32428
amine oxidase (copper-containing) (EC 1.4.3.6) - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 12-Oct-1989 #sequence_revision 31-Dec-1993 #text_change 06-Sep-1996
C;Accession: A32428
R;van der Meer, R.A.; van Wassenaar, P.D.; van Brouwershaven, J.H.; Duine, J.A.
Biochem. Biophys. Res. Commun. 159, 726-733, 1989
A;Title: Primary structure of a pyrroloquinoline quinone (PQQ) containing peptide isolat
A;Reference number: A32428; MUID:89193662; PMID:2539124
A;Accession: A32428
A;Molecule type: protein
A;Residues: 1-7,'K',9-11 <VAN>
A;Note: the modified residue thought by the authors to be pyrroloquinoline quinone coval
C;Keywords: oxidoreductase; quinoprotein; topaquinone
F;8/Modified site: topaquinone (Tyr) #status predicted

  Query Match           26.2%;  Score 16;  DB 2;  Length 11;
  Best Local Similarity   37.5%;  Pred. No. 5.3e+03;
  Matches    3;  Conservative    2;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          3 SEIQFMHN 10
              |:  | :|
Db          2 SDAVFTYN 9
```

RESULT 14
S29735
polyphosphate-glucose phosphotransferase (EC 2.7.1.63) - Propionibacterium freudenreichi
C;Species: Propionibacterium freudenreichii subsp. shermanii
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 03-Jun-2002
C;Accession: S29735
R;Phillips, N.F.B.; Horn, P.J.; Wood, H.G.
Arch. Biochem. Biophys. 300, 309-319, 1993
A;Title: The polyphosphate- and ATP-dependent glucokinase from Propionibacterium sherman
A;Reference number: S29735; MUID:93143332; PMID:8380966
A;Accession: S29735
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-7 <PHI>
C;Keywords: phosphotransferase

Query Match 24.6%; Score 15; DB 2; Length 7;
Best Local Similarity 75.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 HNLG 12
| ||
Db 2 HVLG 5

RESULT 15
PT0231
Ig heavy chain CDR3 region (clone 1-118B) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C;Accession: PT0231
R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity and j
A;Reference number: PT0222; MUID:91108337; PMID:1899102
A;Accession: PT0231
A;Molecule type: DNA
A;Residues: 1-9 <YAM>
A;Experimental source: B lymphocyte
C;Keywords: heterotetramer; immunoglobulin

Query Match 24.6%; Score 15; DB 2; Length 9;
Best Local Similarity 33.3%; Pred. No. 2.8e+05;
Matches 2; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 7 FMHNLG 12
: |: |
Db 1 YTHSSG 6

Search completed: September 5, 2004, 09:37:44
Job time : 10.5 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: September 5, 2004, 09:27:07 ; Search time 6.5 Seconds
(without alignments)
96.130 Million cell updates/sec

Title: US-09-730-174A-4
Perfect score: 61
Sequence: 1 SVSEIQFMHNLG 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 501

Minimum DB seq length: 0
Maximum DB seq length: 12

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	23	37.7	10	1	PSBF_CAPAN	Q03367 capsicum an
2	18	29.5	7	1	LANC_CARUI	P36960 carnobacter
3	18	29.5	10	1	HTF1_ROMMI	P18110 romalea mic
4	16	26.2	8	1	ALL6_CYDPO	P82157 cydia pomon
5	16	26.2	10	1	HTF2_CARMO	P11385 carausius m
6	15	24.6	5	1	EI03_LITRU	P82099 litoria rub
7	15	24.6	8	1	FUSS_FUSSO	P81010 fusarium so
8	15	24.6	10	1	RRPL_PHODV	P35946 phocine dis
9	15	24.6	11	1	EFG_CLOPA	P81350 clostridium
10	15	24.6	11	1	NUHM_CANFA	P49820 canis famil
11	15	24.6	11	1	T2P1_PROVU	P31031 proteus vul
12	14	23.0	4	1	FLRN_ANTEL	P58707 anthopleura
13	14	23.0	7	1	ALL7_CYDPO	P82158 cydia pomon
14	14	23.0	7	1	TY51_LITRU	P82065 litoria rub
15	14	23.0	8	1	AL18_CARMA	P81821 carcinus ma
16	14	23.0	8	1	ALL1_CYDPO	P82152 cydia pomon
17	14	23.0	8	1	HTF1_PERAM	P04548 periplaneta
18	14	23.0	9	1	FAR8_MACRS	P83281 macrobrachi
19	14	23.0	9	1	UF02_MOUSE	P38640 mus musculu
20	14	23.0	10	1	AL19_CARMA	P81822 carcinus ma
21	14	23.0	10	1	TKNC_RANCA	P22690 rana catesb
22	14	23.0	10	1	TKNK_PIG	P01292 sus scrofa
23	14	23.0	11	1	ASL1_BACSE	P83146 bacteroides
24	14	23.0	12	1	HCY1_CARMA	P83176 carcinus ma
25	14	23.0	12	1	LMT1_LOCMI	P22395 locusta mig
26	14	23.0	12	1	PORD_METTM	P80903 methanobact
27	14	23.0	12	1	RS19_TOBBP	Q56251 tomato big
28	13	21.3	6	1	TRPI_PSEPU	P36414 pseudomonas
29	13	21.3	8	1	HTF_TENMO	P25419 tenebrio mo
30	13	21.3	8	1	LCK4_LEUMA	P21143 leucophaea
31	13	21.3	8	1	LCK6_LEUMA	P19988 leucophaea
32	13	21.3	9	1	CONO_CONGE	P05486 conus geogr
33	13	21.3	9	1	MOSH_CLYJA	P19852 clypeaster
34	13	21.3	9	1	OXYT_EISFO	P42998 eisenia foe
35	13	21.3	9	1	PPK1_PERAM	P82691 periplaneta
36	13	21.3	11	1	ASL2_BACSE	P83147 bacteroides
37	13	21.3	11	1	CORZ_PERAM	P11496 periplaneta
38	13	21.3	11	1	CSI5_BACSU	P81095 bacillus su
39	13	21.3	11	1	PVK1_PERAM	P41837 periplaneta
40	13	21.3	11	1	Q2OA_COMTE	P80464 comamonas t
41	13	21.3	12	1	UKA2_HUMAN	P31144 homo sapien
42	13	21.3	12	1	UR2_POLSP	P81022 polyodon sp
43	12	19.7	5	1	RE21_LITRU	P82071 litoria rub
44	12	19.7	5	1	RE31_LITRU	P82072 litoria rub
45	12	19.7	8	1	ANG2_BOTJA	Q10582 bothrops ja

ALIGNMENTS

RESULT 1
PSBF_CAPAN
ID PSBF_CAPAN STANDARD; PRT; 10 AA.
AC Q03367;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Cytochrome b559 beta subunit (PSII reaction center subunit VI)
DE (Fragment).
GN PSBF.
OS Capsicum annuum (Bell pepper).
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC lamiids; Solanales; Solanaceae; Capsicum.
OX NCBI_TaxID=4072;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Lamuyo; TISSUE=Fruit, and Leaf;
RX MEDLINE=93099270; PubMed=1463853;
RA Kuntz M., Camara B., Weil J.-H., Schantz R.;
RT "The psbL gene from bell pepper (Capsicum annuum): plastid RNA
RT editing also occurs in non-photosynthetic chromoplasts.";
RL Plant Mol. Biol. 20:1185-1188(1992).
CC -!- FUNCTION: This b-type cytochrome is tightly associated with the
CC reaction center of photosystem II and possibly is part of the
CC water-oxidation complex.
CC -!- SUBUNIT: Heterodimer of an alpha subunit and a beta subunit.
CC -!- SIMILARITY: Belongs to the psbE / psbF family.
CC --

CC --
DR EMBL; X65570; CAA46539.1; -.
DR PIR; S28055; S28055.
DR HAMAP; MF_00643; -; 1.
DR InterPro; IPR006216; Cyt_b559.
DR PROSITE; PS00537; CYTOCHROME_B559; PARTIAL.
KW Chloroplast; Photosystem II; Heme; Electron transport; Transmembrane.
FT NON_TER 1 1
FT TRANSMEM <1 5 BY SIMILARITY.
FT DOMAIN 6 10 LUMENAL (POTENTIAL).
SQ SEQUENCE 10 AA; 1180 MW; 817D0F59D6D69DC5 CRC64;

Query Match 37.7%; Score 23; DB 1; Length 10;
Best Local Similarity 50.0%; Pred. No. 1.2e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 SVSEIQFM 8
              |:| :||:
Db          1 SISAMQFI 8
```

```
RESULT 2
LANC_CARUI
ID   LANC_CARUI     STANDARD;      PRT;     7 AA.
AC   P36960;
DT   01-JUN-1994 (Rel. 29, Created)
DT   01-JUN-1994 (Rel. 29, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Lantibiotic carnocin UI49 (Fragment).
OS   Carnobacterium sp. (strain UI49).
OC   Bacteria; Firmicutes; Lactobacillales; Carnobacteriaceae;
OC   Carnobacterium.
OX   NCBI_TaxID=35782;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=92321768; PubMed=1622206;
RA   Stoffels G., Nissen-Meyer J., Gudmundsdottir A., Sletten K., Holo H.,
RA   Nes I.F.;
RT   "Purification and characterization of a new bacteriocin isolated from
RT   a Carnobacterium sp.";
RL   Appl. Environ. Microbiol. 58:1417-1422(1992).
CC   -!- FUNCTION: Lanthionine-containing peptide antibiotic (lantibiotic).
CC       Active on Gram-positive bacteria.
KW   Antibiotic; Bacteriocin; Lantibiotic.
FT   NON_TER       7      7
SQ   SEQUENCE   7 AA;  786 MW;  741776D05B05B810 CRC64;

  Query Match             29.5%;  Score 18;  DB 1;  Length 7;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+05;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 SEIQ 6
              ||||
Db          2 SEIQ 5


RESULT 3
HTF1_ROMMI
ID   HTF1_ROMMI     STANDARD;      PRT;    10 AA.
AC   P18110;
DT   01-NOV-1990 (Rel. 16, Created)
DT   01-FEB-1994 (Rel. 28, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   RO I (Hypertrehalosaemic factor).
OS   Romalea microptera (Lubber grasshopper).
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
OC   Acridoidea; Romaleidae; Romalea.
OX   NCBI_TaxID=7007;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Corpora cardiaca;
RX   MEDLINE=89145002; PubMed=3226948;
RA   Gaede G., Hilbich C., Beyreuther K., Rinehart K.L. Jr.;
RT   "Sequence analyses of two neuropeptides of the AKH/RPCH-family from
RT   the lubber grasshopper, Romalea microptera.";
RL   Peptides 9:681-688(1988).
CC   -!- FUNCTION: Hypertrehalosaemic factors are neuropeptides that
CC       elevate the level of trehalose in the hemolymph (trehalose is the
CC       major carbohydrate in the hemolymph of insects).
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: Belongs to the AKH / HRTH / RPCH family.
DR   InterPro; IPR002047; AKH.
DR   PROSITE; PS00256; AKH; 1.
KW   Neuropeptide; Amidation; Flight; Pyrrolidone carboxylic acid.
FT   MOD_RES       1      1       PYRROLIDONE CARBOXYLIC ACID.
FT   MOD_RES      10     10       AMIDATION.
SQ   SEQUENCE   10 AA;  1163 MW;  056236745771A9C4 CRC64;

  Query Match             29.5%;  Score 18;  DB 1;  Length 10;
  Best Local Similarity   33.3%;  Pred. No. 1.1e+03;
  Matches    3;  Conservative    2;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          4 EIQFMHNLG 12
              :: |   | |
Db          1 QVNFTPNWG 9


RESULT 4
ALL6_CYDPO
ID   ALL6_CYDPO     STANDARD;      PRT;     8 AA.
AC   P82157;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   Cydiastatin 6.
OS   Cydia pomonella (Codling moth).
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC   Tortricoidea; Tortricidae; Olethreutinae; Cydia.
OX   NCBI_TaxID=82600;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Larva;
RX   MEDLINE=98054539; PubMed=9392829;
RA   Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Winstanley D.,
RA   Davey M., East P.D., Thorpe A.;
RT   "Lepidopteran peptides of the allatostatin superfamily.";
RL   Peptides 18:1301-1309(1997).
CC   -!- SIMILARITY: Belongs to the allatostatin family.
KW   Neuropeptide; Amidation.
FT   MOD_RES       8      8       AMIDATION.
SQ   SEQUENCE   8 AA;  936 MW;  0B2879C45B573767 CRC64;

  Query Match             26.2%;  Score 16;  DB 1;  Length 8;
  Best Local Similarity   40.0%;  Pred. No. 1.4e+05;
  Matches    2;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          8 MHNLG 12
              ::| |
Db          3 LYNFG 7


RESULT 5
HTF2_CARMO
ID   HTF2_CARMO     STANDARD;      PRT;    10 AA.
AC   P11385;
DT   01-JUL-1989 (Rel. 11, Created)
DT   01-FEB-1994 (Rel. 28, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Hypertrehalosaemic factor II (HTF-II) (HRTH-II) (Hypertrehalosaemic
DE   neuropeptide II).
OS   Carausius morosus (Indian stick insect), and
OS   Extatosoma tiaratum (Stick insect).
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Orthopteroidea; Phasmatodea; Euphasmida; Phasmatoidea;
OC   Heteronemiidae; Carausius.
OX   NCBI_TaxID=7022, 7024;
RN   [1]
RP   SEQUENCE.
RC   SPECIES=C.morosus; TISSUE=Corpora cardiaca;
RX   MEDLINE=87157103; PubMed=3828078;
RA   Gaede G., Rinehart K.L. Jr.;
RT   "Primary structure of the hypertrehalosaemic factor II from the
RT   corpus cardiacum of the Indian stick insect, Carausius morosus,
RT   determined by fast atom bombardment mass spectrometry.";
RL   Biol. Chem. Hoppe-Seyler 368:67-75(1987).
RN   [2]
RP   SEQUENCE.
RC   SPECIES=E.tiaratum; TISSUE=Corpora cardiaca;
RX   MEDLINE=90253659; PubMed=2340112;
RA   Gaede G., Rinehart K.L. Jr.;
RT   "Primary structures of hypertrehalosaemic neuropeptides isolated from
RT   the corpora cardiaca of the cockroaches Leucophaea maderae,
RT   Gromphadorhina portentosa, Blattella germanica and Blatta orientalis
```

```
RT   and of the stick insect Extatosoma tiaratum assigned by tandem fast
RT   atom bombardment mass spectrometry.";
RL   Biol. Chem. Hoppe-Seyler 371:345-354(1990).
RN   [3]
RP   CARBOHYDRATE-LINKAGE SITE.
RC   SPECIES=C.morosus; TISSUE=Corpora cardiaca;
RX   MEDLINE=93129188; PubMed=1482345;
RA   Gaede G., Kellner R., Rinehart K.L. Jr., Proefke M.L.;
RT   "A tryptophan-substituted member of the AKH/RPCH family isolated from
RT   a stick insect corpus cardiacum.";
RL   Biochem. Biophys. Res. Commun. 189:1303-1309(1992).
CC   -!- FUNCTION: Hypertrehalosaemic factors are neuropeptides that
CC       elevate the level of trehalose in the hemolymph (trehalose is the
CC       major carbohydrate in the hemolymph of insects).
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- MASS SPECTROMETRY: MW=1308.61; METHOD=FAB.
CC   -!- SIMILARITY: Belongs to the AKH / HRTH / RPCH family.
DR   PIR; JC1416; JC1416.
DR   PIR; S09138; S09138.
DR   InterPro; IPR002047; AKH.
DR   PROSITE; PS00256; AKH; 1.
KW   Neuropeptide; Amidation; Glycoprotein; Pyrrolidone carboxylic acid.
FT   MOD_RES       1      1       PYRROLIDONE CARBOXYLIC ACID.
FT   CARBOHYD      8      8       C-LINKED (MAN) (PROBABLE).
FT   MOD_RES       10     10      AMIDATION.
SQ   SEQUENCE   10 AA;  1164 MW;  9B9036745771A9D1 CRC64;

  Query Match             26.2%;  Score 16;  DB 1;  Length 10;
  Best Local Similarity   33.3%;  Pred. No. 2.7e+03;
  Matches    3;  Conservative    2;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          4 EIQFMHNLG 12
              :: |  | | |
Db          1 QLTFTPNWG 9


RESULT 6
EI03_LITRU
ID   EI03_LITRU     STANDARD;      PRT;     5 AA.
AC   P82099;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Electrin 3.
OS   Litoria rubella (Desert tree frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae;
OC   Pelodryadinae; Litoria.
OX   NCBI_TaxID=104895;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Skin secretion;
RA   Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
RT   "Peptides from the skin glands of the Australian buzzing tree frog
RT   Litori electrica. Comparison with the skin peptides from Litoria
RT   rubella.";
RL   Aust. J. Chem. 52:639-645(1999).
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- TISSUE SPECIFICITY: Skin.
KW   Amphibian defense peptide; Amidation.
FT   MOD_RES       5      5       AMIDATION.
SQ   SEQUENCE   5 AA;  630 MW;  668761F2C9A00000 CRC64;

  Query Match             24.6%;  Score 15;  DB 1;  Length 5;
  Best Local Similarity   66.7%;  Pred. No. 1.4e+05;
  Matches    2;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 FMH 9
              |:|
Db          1 FVH 3


RESULT 7
FUSS_FUSSO
ID   FUSS_FUSSO     STANDARD;      PRT;     8 AA.
AC   P81010;
DT   15-JUL-1998 (Rel. 36, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Allergen Fus s I3596* (Fragment).
OS   Fusarium solani (subsp. pisi) (Nectria haematococca).
OC   Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC   Hypocreomycetidae; Hypocreales; Nectriaceae; Nectria.
OX   NCBI_TaxID=70791;
RN   [1]
RP   SEQUENCE.
RC   STRAIN=IARI 3596; TISSUE=Mycelium;
RA   Verma J., Gangal S.V.;
RL   Submitted (JUL-1997) to Swiss-Prot.
CC   -!- ALLERGEN: Causes an allergic reaction in human.
KW   Allergen.
FT   NON_TER       8      8
SQ   SEQUENCE   8 AA;  898 MW;  C372C441F5B69041 CRC64;

  Query Match             24.6%;  Score 15;  DB 1;  Length 8;
  Best Local Similarity   66.7%;  Pred. No. 1.4e+05;
  Matches    2;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          9 HNL 11
              ||:
Db          5 HNV 7


RESULT 8
RRPL_PHODV
ID   RRPL_PHODV     STANDARD;      PRT;    10 AA.
AC   P35946;
DT   01-JUN-1994 (Rel. 29, Created)
DT   01-JUN-1994 (Rel. 29, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   RNA polymerase beta subunit (EC 2.7.7.48) (Large structural protein)
DE   (L protein) (Fragment).
GN   L.
OS   Phocine distemper virus (PDV).
OC   Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC   Paramyxoviridae; Paramyxovirinae; Morbillivirus.
OX   NCBI_TaxID=11240;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Ulster/88;
RX   MEDLINE=92268877; PubMed=1588321;
RA   Curran M.D., O'Loan D., Kennedy S., Rima B.K.;
RT   "Molecular characterization of phocine distemper virus: gene order
RT   and sequence of the gene encoding the attachment (H) protein.";
RL   J. Gen. Virol. 73:1189-1194(1992).
CC   -!- FUNCTION: Probable component of the active polymerase. It may
CC       function in mRNA synthesis, capping, methylation and poly(A)
CC       synthesis of newly synthesized viral mRNAs, RNA editing of the P
CC       gene transcript, and protein kinase activity.
CC   -!- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
CC       {RNA}(N).
CC   -!- SIMILARITY: Belongs to the paramyxoviruses L protein family.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; D10371; BAA01208.1; -.
KW   Transferase; RNA-directed RNA polymerase.
FT   NON_TER       10     10
SQ   SEQUENCE   10 AA;  1105 MW;  9C2B7FD452D5A2D5 CRC64;
```

```
  Query Match             24.6%;  Score 15;  DB 1;  Length 10;
  Best Local Similarity   60.0%;  Pred. No. 4.3e+03;
  Matches    3;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SVSEI 5
              ||::|
Db          5 SVNQI 9


RESULT 9
EFG_CLOPA
ID   EFG_CLOPA      STANDARD;      PRT;    11 AA.
AC   P81350;
DT   15-JUL-1998 (Rel. 36, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Elongation factor G (EF-G) (CP 5) (Fragment).
GN   FUSA.
OS   Clostridium pasteurianum.
OC   Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC   Clostridium.
OX   NCBI_TaxID=1501;
RN   [1]
RP   SEQUENCE.
RC   STRAIN=W5;
RX   MEDLINE=98291870; PubMed=9629918;
RA   Flengsrud R., Skjeldal L.;
RT   "Two-dimensional gel electrophoresis separation and N-terminal
RT   sequence analysis of proteins from Clostridium pasteurianum W5.";
RL   Electrophoresis 19:802-806(1998).
CC   -!- FUNCTION: This protein promotes the GTP-dependent translocation of
CC       the nascent protein chain from the A-site to the P-site of the
CC       ribosome.
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC   -!- SIMILARITY: Belongs to the GTP-binding elongation factor family.
CC       EF-G/EF-2 subfamily.
DR   InterPro; IPR000795; EF_GTPbind.
DR   PROSITE; PS00301; EFACTOR_GTP; PARTIAL.
KW   Elongation factor; Protein biosynthesis; GTP-binding.
FT   NON_TER      11     11
SQ   SEQUENCE   11 AA;  1337 MW;  412E71F1D9C33B17 CRC64;

  Query Match             24.6%;  Score 15;  DB 1;  Length 11;
  Best Local Similarity   25.0%;  Pred. No. 4.7e+03;
  Matches    2;  Conservative    3;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          5 IQFMHNLG 12
              ::   |:|
Db          4 LEKFQNIG 11


RESULT 10
NUHM_CANFA
ID   NUHM_CANFA     STANDARD;      PRT;    11 AA.
AC   P49820;
DT   01-OCT-1996 (Rel. 34, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   NADH-ubiquinone oxidoreductase 24 kDa subunit (EC 1.6.5.3)
DE   (EC 1.6.99.3) (Fragment).
GN   NDUFV2.
OS   Canis familiaris (Dog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX   NCBI_TaxID=9615;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Heart;
RX   MEDLINE=98163340; PubMed=9504812;
RA   Dunn M.J., Corbett J.M., Wheeler C.H.;
RT   "HSC-2DPAGE and the two-dimensional gel electrophoresis database of
RT   dog heart proteins.";
RL   Electrophoresis 18:2795-2802(1997).
CC   -!- FUNCTION: TRANSFER OF ELECTRONS FROM NADH TO THE RESPIRATORY
CC       CHAIN. THE IMMEDIATE ELECTRON ACCEPTOR FOR THE ENZYME IS BELIEVED
CC       TO BE UBIQUINONE. COMPONENT OF THE FLAVOPROTEIN-SULFUR (FP)
CC       FRAGMENT OF THE ENZYME.
CC   -!- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
CC   -!- CATALYTIC ACTIVITY: NADH + acceptor = NAD(+) + reduced acceptor.
CC   -!- COFACTOR: Binds 1 2Fe-2S cluster (Potential).
CC   -!- SUBUNIT: Mammalian complex I is composed of 45 different subunits.
CC   -!- SUBCELLULAR LOCATION: Matrix and cytoplasmic side of the
CC       mitochondrial inner membrane.
CC   -!- SIMILARITY: Belongs to the complex I 24 kDa subunit family.
DR   HSC-2DPAGE; P49820; DOG.
DR   InterPro; IPR002023; Cmplx1_24kDa.
DR   PROSITE; PS01099; COMPLEX1_24K; PARTIAL.
KW   Oxidoreductase; NAD; Ubiquinone; Mitochondrion; Metal-binding;
KW   Iron-sulfur; Iron; 2Fe-2S.
FT   NON_TER      11     11
SQ   SEQUENCE   11 AA;  1099 MW;  267F5369C9C72DD8 CRC64;

  Query Match             24.6%;  Score 15;  DB 1;  Length 11;
  Best Local Similarity   66.7%;  Pred. No. 4.7e+03;
  Matches    2;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 FMH 9
              |:|
Db          7 FVH 9


RESULT 11
T2P1_PROVU
ID   T2P1_PROVU     STANDARD;      PRT;    11 AA.
AC   P31031;
DT   01-JUL-1993 (Rel. 26, Created)
DT   01-JUL-1993 (Rel. 26, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Type II restriction enzyme PvuI (EC 3.1.21.4) (Endonuclease PvuI)
DE   (R.PvuI) (Fragment).
GN   PVUIR.
OS   Proteus vulgaris.
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC   Enterobacteriaceae; Proteus.
OX   NCBI_TaxID=585;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=ATCC 13315;
RX   MEDLINE=93087186; PubMed=1454536;
RA   Smith M.D., Longo M., Gerard G.F., Chatterjee D.K.;
RT   "Cloning and characterization of genes for the PvuI restriction and
RT   modification system.";
RL   Nucleic Acids Res. 20:5743-5747(1992).
CC   -!- FUNCTION: RECOGNIZES THE DOUBLE-STRANDED SEQUENCE CGATCG AND
CC       CLEAVES AFTER T-4.
CC   -!- CATALYTIC ACTIVITY: Endonucleolytic cleavage of DNA to give
CC       specific double-stranded fragments with terminal 5'-phosphates.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; L04163; AAA25660.1; -.
DR   PIR; S35490; S35490.
DR   REBASE; 1541; PvuI.
KW   Restriction system; Hydrolase; Nuclease; Endonuclease.
FT   NON_TER      1      1
SQ   SEQUENCE   11 AA;  1300 MW;  9F0CDE7955B72B1A CRC64;

  Query Match             24.6%;  Score 15;  DB 1;  Length 11;
  Best Local Similarity   60.0%;  Pred. No. 4.7e+03;
  Matches    3;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;
```

```
Qy          1 SVSEI 5
              || |:
Db          2 SVDEL 6
```

```
RESULT 12
FLRN_ANTEL
ID   FLRN_ANTEL     STANDARD;      PRT;     4 AA.
AC   P58707;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Antho-RNamide.
OS   Anthopleura elegantissima (Sea anemone).
OC   Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria;
OC   Nynantheae; Actiniidae; Anthopleura.
OX   NCBI_TaxID=6110;
RN   [1]
RP   SEQUENCE, AND MASS SPECTROMETRY.
RX   MEDLINE=90319122; PubMed=1973541;
RA   Grimmelikhuijzen C.J.P., Rinehart K.L. Jr., Jacob E., Graff D.,
RA   Reinscheid R.K., Nothacker H.-P., Staley A.L.;
RT   "Isolation of L-3-phenyllactyl-Leu-Arg-Asn-NH2 (Antho-RNamide), a sea
RT   anemone neuropeptide containing an unusual amino-terminal blocking
RT   group.";
RL   Proc. Natl. Acad. Sci. U.S.A. 87:5410-5414(1990).
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- TISSUE SPECIFICITY: Neuron specific.
CC   -!- MASS SPECTROMETRY: MW=549.3; METHOD=FAB.
DR   PIR; A35779; A35779.
KW   Neuropeptide; Amidation.
FT   MOD_RES       1      1       L-3-PHENYLLACTYL.
FT   MOD_RES       4      4       AMIDATION.
SQ   SEQUENCE   4 AA;  549 MW;  64540729A0000000 CRC64;

  Query Match             23.0%;  Score 14;  DB 1;  Length 4;
  Best Local Similarity   50.0%;  Pred. No. 1.4e+05;
  Matches    2;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 FMHN 10
              |: |
Db          1 FLRN 4
```

```
RESULT 13
ALL7_CYDPO
ID   ALL7_CYDPO     STANDARD;      PRT;     7 AA.
AC   P82158;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   Cydiastatin 7.
OS   Cydia pomonella (Codling moth).
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC   Tortricoidea; Tortricidae; Olethreutinae; Cydia.
OX   NCBI_TaxID=82600;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Larva;
RX   MEDLINE=98054539; PubMed=9392829;
RA   Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Winstanley D.,
RA   Davey M., East P.D., Thorpe A.;
RT   "Lepidopteran peptides of the allatostatin superfamily.";
RL   Peptides 18:1301-1309(1997).
CC   -!- SIMILARITY: Belongs to the allatostatin family.
KW   Neuropeptide; Amidation.
FT   MOD_RES       7      7       AMIDATION.
SQ   SEQUENCE   7 AA;  873 MW;  672879CABB569350 CRC64;

  Query Match             23.0%;  Score 14;  DB 1;  Length 7;
  Best Local Similarity   40.0%;  Pred. No. 1.4e+05;
  Matches    2;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          8 MHNLG 12
              |:: |
Db          2 MYDFG 6
```

```
RESULT 14
TY51_LITRU
ID   TY51_LITRU     STANDARD;      PRT;     7 AA.
AC   P82065;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Tryptophyllin 5.1.
OS   Litoria rubella (Desert tree frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae;
OC   Pelodryadinae; Litoria.
OX   NCBI_TaxID=104895;
RN   [1]
RP   SEQUENCE, AND MASS SPECTROMETRY.
RC   TISSUE=Skin secretion;
RA   Steinborner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,
RA   Tyler M.J., Wallace J.C.;
RT   "The structure of new peptides from the Australin red tree frog
RT   'Litoria rubella'. The skin peptide profile as a probe for the study
RT   of evolutionary trends of amphibians.";
RL   Aust. J. Chem. 49:955-963(1996).
CC   -!- FUNCTION: May act as a neuromodulator or neurotransmitter.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.
CC   -!- MASS SPECTROMETRY: MW=965; METHOD=FAB.
KW   Amphibian defense peptide; Amidation; Neuropeptide;
KW   Pyrrolidone carboxylic acid.
FT   MOD_RES       1      1       PYRROLIDONE CARBOXYLIC ACID.
FT   MOD_RES       7      7       AMIDATION.
SQ   SEQUENCE   7 AA;  983 MW;  7401E9D3676046B0 CRC64;

  Query Match             23.0%;  Score 14;  DB 1;  Length 7;
  Best Local Similarity   33.3%;  Pred. No. 1.4e+05;
  Matches    2;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          4 EIQFMH 9
              :| : |
Db          1 QIPWFH 6
```

```
RESULT 15
AL18_CARMA
ID   AL18_CARMA     STANDARD;      PRT;     8 AA.
AC   P81821;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   Carcinustatin 18.
OS   Carcinus maenas (Common shore crab) (Green crab).
OC   Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC   Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC   Eubrachyura; Portunoidea; Portunidae; Carcinus.
OX   NCBI_TaxID=6759;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Cerebral ganglion, and Thoracic ganglion;
RX   MEDLINE=98121193; PubMed=9461295;
RA   Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
RA   Thorpe A.;
RT   "Isolation and identification of multiple neuropeptides of the
RT   allatostatin superfamily in the shore crab Carcinus maenas.";
RL   Eur. J. Biochem. 250:727-734(1997).
CC   -!- FUNCTION: May act as a neurotransmitter or neuromodulator.
CC   -!- SIMILARITY: Belongs to the allatostatin family.
KW   Neuropeptide; Amidation; Multigene family.
```

```
FT   MOD_RES       8       8       AMIDATION (POTENTIAL).
SQ   SEQUENCE   8 AA;  919 MW;  C82879D5AB569AB5 CRC64;

  Query Match             23.0%;  Score 14;  DB 1;  Length 8;
  Best Local Similarity   40.0%;  Pred. No. 1.4e+05;
  Matches    2;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          8 MHNLG 12
              |:: |
Db          3 MYSFG 7


Search completed: September  5, 2004, 09:35:03
Job time : 7.5 secs
```

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: September 5, 2004, 09:30:03 ; Search time 27.5 Seconds
(without alignments)
137.681 Million cell updates/sec

Title: US-09-730-174A-4
Perfect score: 61
Sequence: 1 SVSEIQFMHNLG 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 2565

Minimum DB seq length: 0
Maximum DB seq length: 12

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_25:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	24	39.3	11	13	Q9PS71	Q9ps71 agkistrodon
2	19	31.1	8	6	Q9TT78	Q9tt78 canis famil
3	19	31.1	9	12	O92766	O92766 canine dist
4	19	31.1	9	12	O71066	O71066 canine dist
5	19	31.1	12	13	P82081	P82081 limnodynast
6	18	29.5	8	3	O13591	O13591 saccharomyc
7	18	29.5	10	4	Q15342	Q15342 homo sapien
8	18	29.5	12	8	Q8MES0	Q8mes0 anoda crist
9	18	29.5	12	15	Q85631	Q85631 avian carci
10	17	27.9	11	5	Q23876	Q23876 dictyosteli
11	17	27.9	11	8	Q35374	Q35374 paramecium
12	16	26.2	7	6	Q28742	Q28742 oryctolagus
13	16	26.2	7	13	Q8JJ20	Q8jj20 gallus gall
14	16	26.2	8	3	Q05403	Q05403 saccharomyc
15	16	26.2	8	10	Q40659	Q40659 oryza sativ
16	16	26.2	8	13	P82082	P82082 limnodynast
17	16	26.2	8	13	P82083	P82083 limnodynast
18	16	26.2	9	2	Q44377	Q44377 aeromonas t
19	16	26.2	9	2	Q44468	Q44468 aeromonas v
20	16	26.2	9	2	Q8RKU3	Q8rku3 borrelia bu
21	16	26.2	9	2	Q43928	Q43928 aeromonas p
22	16	26.2	9	2	Q44001	Q44001 aeromonas e
23	16	26.2	9	10	Q9FXL0	Q9fxl0 lilium long
24	16	26.2	11	8	Q9GD68	Q9gd68 elaeis guin
25	16	26.2	11	10	P82336	P82336 pisum sativ
26	16	26.2	12	13	P82085	P82085 limnodynast
27	15	24.6	8	4	Q15894	Q15894 homo sapien
28	15	24.6	8	8	Q34909	Q34909 locusta mig
29	15	24.6	8	13	Q90493	Q90493 eopsaltria
30	15	24.6	9	2	Q43960	Q43960 azotobacter
31	15	24.6	9	4	Q15891	Q15891 homo sapien
32	15	24.6	9	10	Q8S3C6	Q8s3c6 glycine max
33	15	24.6	9	10	Q9FEC0	Q9fec0 hordeum vul
34	15	24.6	10	5	P82222	P82222 bombyx mori
35	15	24.6	10	10	Q8GZC8	Q8gzc8 hordeum vul
36	15	24.6	10	11	Q61807	Q61807 mus musculu
37	15	24.6	11	3	Q9UR95	Q9ur95 pichia angu
38	15	24.6	11	4	Q9C057	Q9c057 homo sapien
39	15	24.6	11	6	Q9BDC8	Q9bdc8 pongo pygma
40	15	24.6	11	6	Q9BDQ9	Q9bdq9 gorilla gor
41	15	24.6	11	6	Q9BDD0	Q9bdd0 pan troglod
42	15	24.6	11	6	Q9BDC9	Q9bdc9 pan paniscu
43	15	24.6	12	4	Q9UNV5	Q9unv5 homo sapien
44	14	23.0	7	8	O99182	O99182 gnatholebia
45	14	23.0	8	12	Q91U19	Q91u19 influenza a

ALIGNMENTS

RESULT 1
Q9PS71
ID Q9PS71 PRELIMINARY; PRT; 11 AA.
AC Q9PS71;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Fibrinolytic metalloproteinase (Fragment).
OS Agkistrodon contortrix.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Agkistrodon.
OX NCBI_TaxID=8720;
RN [1]
RP SEQUENCE.
RX MEDLINE=91378546; PubMed=1898066;
RA Guan A.L., Retzios A.D., Henderson G.N., Markland F.S.Jr.;
RT "Purification and characterization of a fibrinolytic enzyme from venom
RT of the southern copperhead snake (Agkistrodon contortrix
RT contortrix).";
RL Arch. Biochem. Biophys. 289:197-207(1991).
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1209 MW; 7CA02D1D41E8772B CRC64;

Query Match 39.3%; Score 24; DB 13; Length 11;
Best Local Similarity 100.0%; Pred. No. 5.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 HNLG 12
||||
Db 7 HNLG 10

RESULT 2
Q9TT78
ID Q9TT78 PRELIMINARY; PRT; 8 AA.
AC Q9TT78;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

```
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   Thymidylate synthase (Fragment).
GN   TS.
OS   Canis familiaris (Dog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX   NCBI_TaxID=9615;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21015404; PubMed=11130975;
RA   Brouillette J.A., Andrew J.R., Venta P.J.;
RT   "Estimate of nucleotide diversity in dogs with a pool-and-sequence
RT   method.";
RL   Mamm. Genome 11:1079-1086(2000).
DR   EMBL; AF202073; AAF20918.1; -.
FT   NON_TER       1      1
FT   NON_TER       8      8
SQ   SEQUENCE   8 AA;  899 MW;  6731A1E059CAA867 CRC64;

  Query Match             31.1%;  Score 19;  DB 6;  Length 8;
  Best Local Similarity   60.0%;  Pred. No. 1e+06;
  Matches    3;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 FMHNL 11
              |:| |
Db          4 FIHTL 8


RESULT 3
O92766
ID   O92766      PRELIMINARY;      PRT;     9 AA.
AC   O92766;
DT   01-NOV-1998 (TrEMBLrel. 08, Created)
DT   01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT   01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE   Fusion protein (Fragment).
GN   F.
OS   Canine distemper virus.
OC   Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC   Paramyxoviridae; Paramyxovirinae; Morbillivirus.
OX   NCBI_TaxID=11232;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Dog #5526/89;
RA   Liermann H., Harder T., Haas L.;
RT   "Genetic analysis of the central untranslated genome region and the
RT   proximal coding part of the F gene of wild-type and vaccine distemper
RT   morbilliviruses.";
RL   Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF026237; AAC09167.1; -.
FT   NON_TER       9      9
SQ   SEQUENCE   9 AA;  1011 MW;  F281732760533441 CRC64;

  Query Match             31.1%;  Score 19;  DB 12;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 1e+06;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 MHN 10
              |||
Db          1 MHN 3


RESULT 4
O71066
ID   O71066      PRELIMINARY;      PRT;     9 AA.
AC   O71066;
DT   01-AUG-1998 (TrEMBLrel. 07, Created)
DT   01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   Fusion protein (Fragment).
GN   F.
OS   Canine distemper virus.
OC   Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC   Paramyxoviridae; Paramyxovirinae; Morbillivirus.
OX   NCBI_TaxID=11232;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Dog #10757/96;
RA   Liermann H., Harder T., Haas L.;
RT   "Genetic analysis of the central untranslated genome region and the
RT   proximal coding part of the F gene of wild-type and vaccine distemper
RT   morbilliviruses.";
RL   Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF026234; AAC09164.1; -.
FT   NON_TER       9      9
SQ   SEQUENCE   9 AA;  1124 MW;  F29D045760440441 CRC64;

  Query Match             31.1%;  Score 19;  DB 12;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 1e+06;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 MHN 10
              |||
Db          1 MHN 3


RESULT 5
P82081
ID   P82081      PRELIMINARY;      PRT;    12 AA.
AC   P82081;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE   DYNASTIN 3.
OS   Limnodynastes terraereginae (Northen banjo frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Myobatrachidae;
OC   Limnodynastinae; Limnodynastes.
OX   NCBI_TaxID=104894;
RN   [1]
RP   SEQUENCE, AND MASS SPECTROMETRY.
RC   TISSUE=TIBIAL GLAND;
RA   Raftery M.J., Bradford A.M., Bowie J.H., Wallace J.C., Tyler M.J.;
RT   "Peptides from Australian frogs. The structure of the dynastins from
RT   the banjo frogs Limnodynastes interioras, Limnodynastes dumerilii and
RT   Limnodynastes terraereginae.";
RL   Aust. J. Chem. 46:833-842(1993).
CC   -!- MASS SPECTROMETRY: MW=1236; METHOD=FAB.
SQ   SEQUENCE   12 AA;  1236 MW;  147AA70FDF472724 CRC64;

  Query Match             31.1%;  Score 19;  DB 13;  Length 12;
  Best Local Similarity   60.0%;  Pred. No. 6.7e+03;
  Matches    3;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 MHNLG 12
              ::|||
Db          7 LNNLG 11


RESULT 6
O13591
ID   O13591      PRELIMINARY;      PRT;     8 AA.
AC   O13591;
DT   01-JAN-1998 (TrEMBLrel. 05, Created)
DT   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT   01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE   ORF YNL337W (Fragment).
OS   Saccharomyces cerevisiae (Baker's yeast).
OC   Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC   Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX   NCBI_TaxID=4932;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Obermaier B., Piravandi E., Rinke M.;
RL   Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
RN   [2]
```

```
RP   SEQUENCE FROM N.A.
RA   MIPS;
RL   Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; Z71612; CAA96271.2; -.
FT   NON_TER       1      1
SQ   SEQUENCE   8 AA;  1005 MW;  5CA441E449C9C720 CRC64;

  Query Match           29.5%;  Score 18;  DB 3;  Length 8;
  Best Local Similarity   75.0%;  Pred. No. 1e+06;
  Matches    3;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 FMHN 10
              | ||
Db          4 FNHN 7


RESULT 7
Q15342
ID   Q15342      PRELIMINARY;      PRT;    10 AA.
AC   Q15342;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Aml1 protein (Fragment).
GN   AML1.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=96226397; PubMed=8634147;
RA   Levanon D., Bernstein Y., Negreanu V., Ghozi M.C., Bar-Am I.,
RA   Aloya R., Goldenberg D., Lotem J., Groner Y.;
RT   "A large variety of alternatively spliced and differentially expressed
RT   mRNAs are encoded by the human acute myeloid leukemia gene AML1.";
RL   DNA Cell Biol. 15:175-185(1996).
DR   EMBL; X90978; CAA62465.1; -.
FT   NON_TER       1      1
SQ   SEQUENCE   10 AA;  1254 MW;  8D99287B441AF365 CRC64;

  Query Match           29.5%;  Score 18;  DB 4;  Length 10;
  Best Local Similarity   44.4%;  Pred. No. 8.8e+03;
  Matches    4;  Conservative    2;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 SVSEIQFMH 9
              |||  :: |
Db          1 SVSWXRYPH 9


RESULT 8
Q8MES0
ID   Q8MES0      PRELIMINARY;      PRT;    12 AA.
AC   Q8MES0;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Ribosomal protein 16 (Fragment).
GN   RPL16.
OS   Anoda cristata.
OG   Chloroplast.
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC   eurosids II; Malvales; Malvaceae; Malvoideae; Anoda.
OX   NCBI_TaxID=183227;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Pfeil B.E., Brubaker C.L., Craven L.A., Crisp M.D.;
RT   "Phylogeny of Hibiscus and the tribe Hibisceae (Malvaceae) using
RT   chloroplast DNA sequences of ndhF and the rpl16 intron.";
RL   Syst. Bot. 27:333-350(2002).
DR   EMBL; AF384567; AAM50405.1; -.
DR   GO; GO:0009507; C:chloroplast; IEA.
KW   Chloroplast.
FT   NON_TER       1      1
FT   NON_TER      12     12
SQ   SEQUENCE   12 AA;  1431 MW;  9A5E59B65452C9CA CRC64;

  Query Match           29.5%;  Score 18;  DB 8;  Length 12;
  Best Local Similarity   37.5%;  Pred. No. 1.1e+04;
  Matches    3;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          4 EIQFMHNL 11
              |  |::|:
Db          3 EPDFVNNI 10


RESULT 9
Q85631
ID   Q85631      PRELIMINARY;      PRT;    12 AA.
AC   Q85631;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   MH2, proviral DNA, myc to 3' LTR (Fragment).
OS   Avian carcinoma virus.
OC   Viruses; Retroid viruses; Retroviridae; Alpharetrovirus.
OX   NCBI_TaxID=11958;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=85033920; PubMed=6092695;
RA   Sutrave P., Jansen H.W., Bister K., Rapp U.R.;
RT   "3'-terminal region of avian carcinoma virus MH2 shares sequence
RT   elements with avian sarcoma viruses Y73 and SR-A.";
RL   J. Virol. 52:703-705(1984).
DR   EMBL; K03100; AAA42388.1; -.
FT   NON_TER       1      1
SQ   SEQUENCE   12 AA;  1466 MW;  72E4B884F30736DB CRC64;

  Query Match           29.5%;  Score 18;  DB 15;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+04;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          9 HNL 11
              |||
Db          2 HNL 4


RESULT 10
Q23876
ID   Q23876      PRELIMINARY;      PRT;    11 AA.
AC   Q23876;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE   Actin 4.
OS   Dictyostelium discoideum (Slime mold).
OC   Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
OX   NCBI_TaxID=44689;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=82260445; PubMed=6286214;
RA   McKeown M., Firtel R.A.;
RT   "Actin multigene family of Dictyostelium.";
RL   Cold Spring Harb. Symp. Quant. Biol. 46:495-505(1982).
DR   EMBL; K02957; AAA33150.1; -.
DR   EMBL; K02956; AAA33150.1; JOINED.
SQ   SEQUENCE   11 AA;  1205 MW;  728B4C14C6C2CAAB CRC64;

  Query Match           27.9%;  Score 17;  DB 5;  Length 11;
  Best Local Similarity   28.6%;  Pred. No. 1.5e+04;
  Matches    2;  Conservative    4;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 EIQFMHN 10
              ::| ::|
Db          5 DVQALNN 11
```

```
RESULT 11
Q35374
ID   Q35374      PRELIMINARY;      PRT;    11 AA.
AC   Q35374;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   P1 protein (Fragment).
OS   Paramecium tetraurelia.
OG   Mitochondrion.
OC   Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Peniculida;
OC   Paramecium.
OX   NCBI_TaxID=5888;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=stock 172;
RX   MEDLINE=87055241; PubMed=3023187;
RA   Pritchard A.E., Seilhamer J.J., Cummings D.J.;
RT   "Paramecium mitochondrial DNA sequences and RNA transcripts for
RT   cytochrome oxidase subunit I, URF1, and three ORFs adjacent to the
RT   replication origin.";
RL   Gene 44:243-253(1986).
DR   EMBL; M15280; AAA79267.1; -.
DR   GO; GO:0005739; C:mitochondrion; IEA.
KW   Mitochondrion.
FT   NON_TER      11     11
SQ   SEQUENCE   11 AA;  1266 MW;  1D84259D16D046D4 CRC64;

  Query Match           27.9%;  Score 17;  DB 8;  Length 11;
  Best Local Similarity   50.0%;  Pred. No. 1.5e+04;
  Matches    3;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SVSEIQ 6
              |:::||
Db          2 SLNQIQ 7


RESULT 12
Q28742
ID   Q28742      PRELIMINARY;      PRT;     7 AA.
AC   Q28742;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Alpha-myosin heavy chain (Fragment).
OS   Oryctolagus cuniculus (Rabbit).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX   NCBI_TaxID=9986;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=84221901; PubMed=6328491;
RA   Friedman D.J., Umeda P.K., Sinha A.M., Hsu H.-J., Jokovcic S.,
RA   Rabinowitz M.;
RT   "Characterization of genomic clones specifying rabbit alpha- and beta-
RT   ventricular myosin heavy chains.";
RL   Proc. Natl. Acad. Sci. U.S.A. 81:3044-3048(1984).
DR   EMBL; K01698; AAA31415.1; -.
DR   PIR; I46868; I46868.
FT   NON_TER      1      1
SQ   SEQUENCE   7 AA;  916 MW;  6B1B1AA1E69326B0 CRC64;

  Query Match           26.2%;  Score 16;  DB 6;  Length 7;
  Best Local Similarity   60.0%;  Pred. No. 1e+06;
  Matches    3;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          6 QFMHN 10
              | ||:
Db          1 QKMHD 5


RESULT 13
Q8JJ20
ID   Q8JJ20      PRELIMINARY;      PRT;     7 AA.
AC   Q8JJ20;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE   Extracellular fatty acid binding protein (Fragment).
GN   EXFABP.
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Blood;
RA   Wang Q., Li N., Li H.;
RT   "Cloning and sequencing of 3' UTR of EXFABP gene in chicken.";
RL   Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF487519; AAL96665.1; -.
FT   NON_TER      1      1
SQ   SEQUENCE   7 AA;  780 MW;  72CB1AB2D5BEBB70 CRC64;

  Query Match           26.2%;  Score 16;  DB 13;  Length 7;
  Best Local Similarity   60.0%;  Pred. No. 1e+06;
  Matches    3;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 SVSEI 5
              || |:
Db          3 SVDEV 7


RESULT 14
Q05403
ID   Q05403      PRELIMINARY;      PRT;     8 AA.
AC   Q05403;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE   DNA for ORF'S from chromosome XV (Fragment).
OS   Saccharomyces cerevisiae (Baker's yeast).
OC   Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC   Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX   NCBI_TaxID=4932;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=FY1679;
RX   MEDLINE=96021609; PubMed=8533473;
RA   Zumstein E., Pearson B.M., Kalogeropoulos A., Schweizer M.;
RT   "A 29.425 kb segment on the left arm of yeast chromosome XV contains
RT   more than twice as many unknown as known open reading frames.";
RL   Yeast 11:975-986(1995).
DR   EMBL; X83121; CAA58183.1; -.
FT   NON_TER      8      8
SQ   SEQUENCE   8 AA;  879 MW;  7B5322D2C441E058 CRC64;

  Query Match           26.2%;  Score 16;  DB 3;  Length 8;
  Best Local Similarity   50.0%;  Pred. No. 1e+06;
  Matches    2;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 MHNL 11
              :||:
Db          2 IHNV 5


RESULT 15
Q40659
ID   Q40659      PRELIMINARY;      PRT;     8 AA.
AC   Q40659;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
```

```
DE   Alpha-amylase (Fragment).
OS   Oryza sativa (Rice).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC   Ehrhartoideae; Oryzeae; Oryza.
OX   NCBI_TaxID=4530;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91078641; PubMed=2258052;
RA   Kumagai M.H., Shah M., Terashima M., Vrkljan Z., Whitaker J.R.,
RA   Rodriquez R.L.;
RT   "Expression and secretion of rice alpha-amylase by saccharomycers
RT   cerevisiae.";
RL   Gene 94:209-216(1990).
DR   EMBL; M62916; AAA33892.1; -.
DR   Gramene; Q40659; -.
FT   NON_TER       8      8
SQ   SEQUENCE   8 AA;  948 MW;  EBC694444732D6D6 CRC64;

  Query Match             26.2%;  Score 16;  DB 10;  Length 8;
  Best Local Similarity   28.6%;  Pred. No. 1e+06;
  Matches    2;  Conservative    4;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          5 IQFMHNL 11
              :|  ::|:
Db          1 MQVLNNM 7


Search completed: September  5, 2004, 09:37:00
Job time : 28.5 secs
```

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: September 5, 2004, 09:26:47 ; Search time 36.5 Seconds
(without alignments)
92.892 Million cell updates/sec

Title: US-09-730-174A-4
Perfect score: 61
Sequence: 1 SVSEIQFMHNLG 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 368311

Minimum DB seq length: 0
Maximum DB seq length: 12

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	50	82.0	11	6	ABG72607	Abg72607 Parathyro
2	50	82.0	12	6	ABG72608	Abg72608 Parathyro
3	46	75.4	11	3	AAY96968	Aay96968 Parathyro
4	45	73.8	10	2	AAR91644	Aar91644 Human par
5	45	73.8	10	3	AAY68767	Aay68767 Amino aci
6	45	73.8	10	4	AAB86219	Aab86219 Human par
7	45	73.8	10	6	ABR44166	Abr44166 Human par
8	41	67.2	9	4	AAB86225	Aab86225 Human par
9	39	63.9	9	2	AAR91645	Aar91645 Human par
10	39	63.9	9	3	AAY96981	Aay96981 Parathyro
11	39	63.9	9	4	AAB86220	Aab86220 Human par
12	38.5	63.1	11	2	AAY50600	Aay50600 Resin bou
13	36	59.0	9	3	AAB01862	Aab01862 PTH(1-14)
14	36	59.0	9	3	AAY96966	Aay96966 Parathyro
15	33	54.1	9	3	AAB01863	Aab01863 PTH(1-14)
16	33	54.1	10	4	AAB96932	Aab96932 Rat parat
17	33	54.1	11	4	AAB96931	Aab96931 Rat parat
18	33	54.1	11	4	AAB96915	Aab96915 Parathyro
19	33	54.1	11	4	AAB84770	Aab84770 Parathyro
20	33	54.1	12	4	AAB96914	Aab96914 Parathyro
21	33	54.1	12	4	AAB84769	Aab84769 Parathyro
22	32	52.5	9	3	AAY78849	Aay78849 Parathyro
23	31	50.8	8	2	AAR91646	Aar91646 Human par
24	31	50.8	8	3	AAB07467	Aab07467 Antigenic
25	31	50.8	8	4	AAB86221	Aab86221 Human par
26	31	50.8	10	6	ABP71484	Abp71484 Parathyro
27	31	50.8	11	6	ABP71485	Abp71485 Parathyro
28	31	50.8	11	6	ABP71483	Abp71483 Parathyro
29	31	50.8	12	2	AAW45785	Aaw45785 Parathyro
30	31	50.8	12	6	ABP71482	Abp71482 Parathyro
31	29	47.5	9	3	AAB01866	Aab01866 PTH(1-14)
32	28	45.9	11	1	AAP82547	Aap82547 (Asn10, T
33	28	45.9	11	4	AAB96892	Aab96892 Rat parat
34	28	45.9	12	4	AAB96891	Aab96891 Rat parat
35	27	44.3	10	5	ABG69386	Abg69386 Vascular
36	27	44.3	11	4	ABU54029	Abu54029 Human DNA
37	26	42.6	6	2	AAR91648	Aar91648 Human par
38	26	42.6	6	3	AAY68764	Aay68764 Amino aci
39	26	42.6	6	4	AAB86223	Aab86223 Human par
40	26	42.6	6	6	ABR44168	Abr44168 Human par
41	26	42.6	7	2	AAR91647	Aar91647 Human par
42	26	42.6	7	3	AAB00068	Aab00068 N-termina
43	26	42.6	7	4	AAB86222	Aab86222 Human par
44	26	42.6	9	3	AAB01864	Aab01864 PTH(1-14)
45	26	42.6	9	3	AAY97062	Aay97062 PTH-rP N-

ALIGNMENTS

RESULT 1
ABG72607
ID ABG72607 standard; peptide; 11 AA.
XX
AC ABG72607;
XX
DT 11-FEB-2003 (first entry)
XX
DE Parathyroid hormone antigenic peptide 2-12.
XX
KW Human; parathyroid hormone; antigen; hypercalcaemia; osteoporosis;
KW primary hyperparathyroidism; mouse; rat; bovine; porcine; canine.
XX
OS Homo sapiens.
OS Mus sp.
OS Rattus sp.
OS Bos taurus.
OS Sus scrofa.
OS Canis familiaris.
XX
FH Key Location/Qualifiers
FT Misc-difference 6
FT /label= Leu, Phe
XX
PN US2002110871-A1.
XX
PD 15-AUG-2002.
XX
PF 05-DEC-2000; 2000US-00730174.
XX
PR 05-DEC-2000; 2000US-00730174.
XX
PA (ZAHR/) ZAHRADNIK R J.
PA (LAVI/) LAVIGNE J R.
XX
PI Zahradnik RJ, Lavigne JR;
XX
DR WPI; 2003-066685/06.
XX
PT New parathyroid hormone (PTH) antigenic peptide inducing the formation
PT and isolation of antibodies having an affinity to it, useful for
PT determining bioactive PTH levels in serum, plasma and/or cell culture
PT media.
XX
PS Claim 1; Page 5; 11pp; English.
XX
CC The invention relates to a new antigenic peptide for inducing the
CC formation and isolation of antibodies having an affinity to it, being

CC formed from the N-terminus of parathyroid hormone (PTH). Also included
CC are; (1) a method for producing antibodies useful in the determination of
CC PTH levels in a biological sample comprising: (a) providing at least one
CC first peptide antigen comprising a peptide fragment of PTH; (b)
CC administering the first peptide antigen to a host animal to induce
CC antibody production; (c) monitoring the antibody titre produced; (d)
CC isolating antisera produced in the host animal; and (e) selecting
CC antisera from the isolated antisera produced in the host that is capable
CC of binding to a second peptide antigen; (2) an antibody (ab) produced by
CC the method; and (3) test kits and analytical procedures used for the
CC determination of bioactive intact PTH utilising (ab). The methods and
CC compositions of the present invention are useful for determining
CC bioactive intact PTH levels in serum, plasma and/or cell culture media.
CC The antigens, antibodies and methods of the present invention, as
CC compared to prior art, have the particular advantages of possessing
CC greater affinity for PTH, and in particular, are designed to have a novel
CC recognition for amino acid residues extending beyond the first N-terminal
CC PTH residue, and further have negligible cross-reactivity with the large
CC non-molecular forms of PTH. PTH levels are an important parameter in
CC patients suffering from hypercalcaemia, osteoporosis and primary
CC hyperparathyroidism. The present sequence represents a PTH antigenic
CC peptide representing amino acids 2-12 of human, mouse, rat, porcine,
CC canine and bovine PTH
XX
SQ Sequence 11 AA;

Query Match 82.0%; Score 50; DB 6; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.01;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 VSEIQFMHNLG 12
||||| |||||
Db 1 VSEIQXMHNLG 11

RESULT 2
ABG72608
ID ABG72608 standard; peptide; 12 AA.
XX
AC ABG72608;
XX
DT 11-FEB-2003 (first entry)
XX
DE Parathyroid hormone antigenic peptide 1-12.
XX
KW Human; parathyroid hormone; antigen; hypercalcaemia; osteoporosis;
KW primary hyperparathyroidism; mouse; rat; bovine; porcine; canine.
XX
OS Homo sapiens.
OS Mus sp.
OS Rattus sp.
OS Bos taurus.
OS Sus scrofa.
OS Canis familiaris.
XX
FH Key Location/Qualifiers
FT Misc-difference 1
FT /label= Ser, Ala
FT Misc-difference 7
FT /label= Leu, Phe
XX
PN US2002110871-A1.
XX
PD 15-AUG-2002.
XX
PF 05-DEC-2000; 2000US-00730174.
XX
PR 05-DEC-2000; 2000US-00730174.
XX
PA (ZAHR/) ZAHRADNIK R J.
PA (LAVI/) LAVIGNE J R.
XX
PI Zahradnik RJ, Lavigne JR;

XX
DR WPI; 2003-066685/06.
XX
PT New parathyroid hormone (PTH) antigenic peptide inducing the formation
PT and isolation of antibodies having an affinity to it, useful for
PT determining bioactive PTH levels in serum, plasma and/or cell culture
PT media.
XX
PS Claim 2; Page 5; 11pp; English.
XX
CC The invention relates to a new antigenic peptide for inducing the
CC formation and isolation of antibodies having an affinity to it, being
CC formed from the N-terminus of parathyroid hormone (PTH). Also included
CC are; (1) a method for producing antibodies useful in the determination of
CC PTH levels in a biological sample comprising: (a) providing at least one
CC first peptide antigen comprising a peptide fragment of PTH; (b)
CC administering the first peptide antigen to a host animal to induce
CC antibody production; (c) monitoring the antibody titre produced; (d)
CC isolating antisera produced in the host animal; and (e) selecting
CC antisera from the isolated antisera produced in the host that is capable
CC of binding to a second peptide antigen; (2) an antibody (ab) produced by
CC the method; and (3) test kits and analytical procedures used for the
CC determination of bioactive intact PTH utilising (ab). The methods and
CC compositions of the present invention are useful for determining
CC bioactive intact PTH levels in serum, plasma and/or cell culture media.
CC The antigens, antibodies and methods of the present invention, as
CC compared to prior art, have the particular advantages of possessing
CC greater affinity for PTH, and in particular, are designed to have a novel
CC recognition for amino acid residues extending beyond the first N-terminal
CC PTH residue, and further have negligible cross-reactivity with the large
CC non-molecular forms of PTH. PTH levels are an important parameter in
CC patients suffering from hypercalcaemia, osteoporosis and primary
CC hyperparathyroidism. The present sequence represents a PTH antigenic
CC peptide representing amino acids 1-12 of human, mouse, rat, porcine,
CC canine and bovine PTH
XX
SQ Sequence 12 AA;

Query Match 82.0%; Score 50; DB 6; Length 12;
Best Local Similarity 90.9%; Pred. No. 0.011;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 VSEIQFMHNLG 12
||||| |||||
Db 2 VSEIQXMHNLG 12

RESULT 3
AAY96968
ID AAY96968 standard; peptide; 11 AA.
XX
AC AAY96968;
XX
DT 31-OCT-2000 (first entry)
XX
DE Parathyroid hormone N-terminal signaling domain (residues 1-11).
XX
KW PTH; parathyroid hormone; N-terminal; signaling domain; bone mass;
KW bone reformation; resorption; remodeling; tether1; osteoporosis.
XX
OS Homo sapiens.
XX
PN WO200039278-A2.
XX
PD 06-JUL-2000.
XX
PF 30-DEC-1999; 99WO-US031108.
XX
PR 31-DEC-1998; 98US-0114577P.
XX
PA (GARD/) GARDELLA T J.
PA (KRON/) KRONENBERG H M.
PA (POTT/) POTTS J T.

PA (JUEP/) JUEPPNER H.
XX
PI Gardella TJ, Kronenberg HM, Potts JT, Jueppner H;
XX
DR WPI; 2000-452384/39.
XX
PT New compound comprising an amino terminal signaling functional domain
PT linked to a carboxy-terminal binding portion of parathyroid hormone for
PT treating mammalian conditions characterized by decreases in bone mass.
XX
PS Claim 4; Page 92; 119pp; English.
XX
CC Compounds of the structure or formula S-(L)_n-B, R_1-S-(L)_n-R or S-(L)_n
CC -R, are new. S is an amino terminal signaling functional domain of
CC parathyroid hormone (PTH); L is a linker molecule present n times (where
CC n is a positive integer 1-10 (preferably 4)); B is a C-terminal binding
CC portion of PTH(1-34) or a PTH-related protein (PTH-rP) (1-34); R_1 is the
CC PTH-1 receptor signal sequence; and R is (a portion of) PTH-1 receptor
CC sequence. The new compounds are used for treating mammalian conditions
CC characterized by decreases in bone mass, determining rates of bone
CC reformation, bone resorption and/or bone remodeling, treating diseases
CC and disorders associated with decreased tetherl activity, increasing cAMP
CC in a mammalian cell having PTH-1 receptors, or screening for a peptide or
CC non-peptide PTH (claimed). The new compound can be administered by
CC inhalation unlike the large native PTH or PTHrP which avoids the need for
CC regular injections to treat osteoporosis
XX
SQ Sequence 11 AA;

Query Match 75.4%; Score 46; DB 3; Length 11;
Best Local Similarity 81.8%; Pred. No. 0.059;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SVSEIQFMHNL 11
:||||| ||||
Db 1 AVSEIQLMHNL 11

RESULT 4
AAR91644
ID AAR91644 standard; peptide; 10 AA.
XX
AC AAR91644;
XX
DT 06-NOV-1996 (first entry)
XX
DE Human parathyroid hormone antigenic peptide hPTH 1-10.
XX
KW Human parathyroid hormone; hPTH; antigen; alpha-helix; immunogen;
KW diagnosis; active hPTH 1-37.
XX
OS Synthetic.
XX
PN DE4434551-A1.
XX
PD 04-APR-1996.
XX
PF 28-SEP-1994; 94DE-04434551.
XX
PR 28-SEP-1994; 94DE-04434551.
XX
PA (FORS/) FORSSMANN W.
XX
PI Adermann K, Forssmann W, Hock D, Maegerlein M;
XX
DR WPI; 1996-180391/19.
XX
PT New antigenic peptide(s) from human parathyroid hormone - and antibodies
PT generated using them, able to distinguish between active and inactive
PT forms of the hormone.
XX
PS Claim 2; Page 4; 5pp; German.
XX
CC The present sequence is a specific example of claimed immunogenic
CC peptides having a sequence from hPTH(1-37) which includes the N- or C-
CC terminal alpha-helical region and/or the non-structured region of the
CC hormone. Antibodies and their binding fragments generated by injecting an
CC animal with the peptides are useful as diagnostic reagents for
CC determination of biologically active hPTH(1-37)
XX
SQ Sequence 10 AA;

Query Match 73.8%; Score 45; DB 2; Length 10;
Best Local Similarity 90.0%; Pred. No. 0.082;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SVSEIQFMHN 10
|||||| |||
Db 1 SVSEIQLMHN 10

RESULT 5
AAY68767
ID AAY68767 standard; peptide; 10 AA.
XX
AC AAY68767;
XX
DT 05-MAY-2000 (first entry)
XX
DE Amino acids 1-10 of a parathyroid hormone (pTH).
XX
KW Parathyroid hormone; lipolysis; cosmetic; dermatological; skin care;
KW slimming treatment; cellulite; skin firming.
XX
OS Unidentified.
XX
PN WO200004047-A1.
XX
PD 27-JAN-2000.
XX
PF 07-JUL-1999; 99WO-FR001687.
XX
PR 17-JUL-1998; 98FR-00009193.
XX
PA (SEDE-) SEDERMA.
XX
PI Lintner K;
XX
DR WPI; 2000-171243/15.
XX
PT New parathyroid hormone fragment peptides, used as lipolysis stimulants
PT in topically applied cosmetic compositions for slimming treatment of
PT excessive weight in hips and thighs.
XX
PS Claim 1; Page 8; 18pp; French.
XX
CC The present sequence represents a parathyroid hormone (pTH) fragment,
CC comprising amino acids 1-10. Parathyroid hormone fragments of the
CC invention have lipolysis stimulating activity (especially when topically
CC administered). The lipolytic activity of the peptides is enhanced when
CC they are chemically modified to increase their lipophilicity. The
CC peptides are used in cosmetic or dermatological compositions for skin
CC care. They are especially used for slimming treatment of excessive weight
CC in the thighs and hips, in the treatment of cellulite and for skin
CC firming
XX
SQ Sequence 10 AA;

Query Match 73.8%; Score 45; DB 3; Length 10;
Best Local Similarity 90.0%; Pred. No. 0.082;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SVSEIQFMHN 10
|||||| |||
Db 1 SVSEIQLMHN 10

```
RESULT 6
AAB86219
ID   AAB86219 standard; peptide; 10 AA.
XX
AC   AAB86219;
XX
DT   03-SEP-2001  (first entry)
XX
DE   Human parathyroid hormone immunogenic peptide SEQ ID 1.
XX
KW   Parathyroid hormone; hPTH; immunogenic peptide; human; epitope;
KW   diagnosis; calcium-metabolism disorder; osteopathy; antagonist;
KW   hypo-parathyroidism; hyper-parathyroidism.
XX
OS   Homo sapiens.
XX
PN   DE19961350-A1.
XX
PD   21-JUN-2001.
XX
PF   17-DEC-1999;   99DE-01061350.
XX
PR   17-DEC-1999;   99DE-01061350.
XX
PA   (IMMU-) IMMUNDIAGNOSTIK AG.
XX
PI   Armbruster FP;
XX
DR   WPI; 2001-376318/40.
XX
PT   Determining the content of physiologically active parathyroid hormone,
PT   useful in diagnosis of calcium-metabolism disorders, using two antibodies
PT   reactive with different epitopes.
XX
PS   Disclosure; Page 3; 10pp; German.
XX
CC   This invention describes a novel method for determining (M1) the content
CC   of active parathyroid hormone (A) by treating a sample with (i) antibody
CC   (Ab1) that recognizes the epitope formed by amino acids (aa) 1-3 of (A),
CC   and including the N-terminal residue and (ii) antibody (Ab2) that
CC   recognizes an epitope within the receptor-binding site of (A). The number
CC   of molecules that react with both antibodies is determined and used to
CC   calculate the content of physiologically active (A). The method is used
CC   for diagnosis of calcium-metabolism disorders, osteopathy, or hypo- or
CC   hyper-parathyroidism. The method (unlike known assays) recognizes that
CC   (i) some fragments of (A) shorter than the complete (84 aa) peptide are
CC   active and (ii) that apparently intact peptide may be biologically
CC   inactive, and also takes into account the fact that some fragments of (A)
CC   are antagonistic (these have the receptor-binding site but lack the N-
CC   terminus). It thus provides a true measure of the content of
CC   physiologically active (A); contrast methods that measure intact peptide
CC   and its 1-37 fragment which may produce falsely high values. This
CC   sequence represents a peptide fragment used to illustrate the method of
CC   the invention
XX
SQ   Sequence 10 AA;

  Query Match             73.8%;  Score 45;  DB 4;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 0.082;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 SVSEIQFMHN 10
              |||||| |||
Db          1 SVSEIQLMHN 10


RESULT 7
ABR44166
ID   ABR44166 standard; peptide; 10 AA.
XX
AC   ABR44166;
XX
DT   04-AUG-2003  (first entry)
XX
DE   Human parathyroid hormone (hPTH) fragment (residues 1-10).
XX
KW   Fusion peptide; tat; hPTHDP; parathyroid hormone; skin; cosmetic;
KW   lipolysis; human; hPTH.
XX
OS   Homo sapiens.
XX
PN   WO2003035697-A1.
XX
PD   01-MAY-2003.
XX
PF   06-MAY-2002; 2002WO-KR000835.
XX
PR   27-SEP-2001; 2001KR-00060245.
PR   15-MAR-2002; 2002KR-00014062.
XX
PA   (GLDS ) LG HOUSEHOLD & HEALTH CARE LTD.
XX
PI   Song Y,  Kang N,  Park S,  Cho W,  Kang S,  Lee Y,  Lim J,  Min H;
PI   Chang M;
XX
DR   WPI; 2003-468288/44.
XX
PT   Novel fusion peptide comprising self cell-penetrating Tat peptide bound
PT   to human parathyroid hormone-derived peptide, useful as component of skin
PT   slimming cosmetic composition.
XX
PS   Claim 5; Page 6; 32pp; English.
XX
CC   The invention relates to a fusion peptide (Tat-hPTHDP), where self cell-
CC   penetrating Tat peptide is bound to human parathyroid hormone-derived
CC   peptide (hPTHDP). The fusion peptide is useful as a component of skin
CC   slimming cosmetic composition. The fusion peptide does not cause
CC   irritation, easily and safely penetrates into integument and endothelium,
CC   does not cause skin disease and has superior lipolysis effects, and is
CC   durable. The present sequence represents a human parathyroid hormone
CC   (hPTH) fragment that can be used to construct the fusion peptide
XX
SQ   Sequence 10 AA;

  Query Match             73.8%;  Score 45;  DB 6;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 0.082;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 SVSEIQFMHN 10
              |||||| |||
Db          1 SVSEIQLMHN 10


RESULT 8
AAB86225
ID   AAB86225 standard; peptide; 9 AA.
XX
AC   AAB86225;
XX
DT   03-SEP-2001  (first entry)
XX
DE   Human parathyroid hormone immunogenic peptide SEQ ID 7.
XX
KW   Parathyroid hormone; hPTH; immunogenic peptide; human; epitope;
KW   diagnosis; calcium-metabolism disorder; osteopathy; antagonist;
KW   hypo-parathyroidism; hyper-parathyroidism.
XX
OS   Homo sapiens.
XX
PN   DE19961350-A1.
XX
PD   21-JUN-2001.
XX
PF   17-DEC-1999;   99DE-01061350.
XX
```

PR 17-DEC-1999; 99DE-01061350.
XX
PA (IMMU-) IMMUNDIAGNOSTIK AG.
XX
PI Armbruster FP;
XX
DR WPI; 2001-376318/40.
XX
PT Determining the content of physiologically active parathyroid hormone,
PT useful in diagnosis of calcium-metabolism disorders, using two antibodies
PT reactive with different epitopes.
XX
PS Disclosure; Page 3; 10pp; German.
XX
CC This invention describes a novel method for determining (M1) the content
CC of active parathyroid hormone (A) by treating a sample with (i) antibody
CC (Ab1) that recognizes the epitope formed by amino acids (aa) 1-3 of (A),
CC and including the N-terminal residue and (ii) antibody (Ab2) that
CC recognizes an epitope within the receptor-binding site of (A). The number
CC of molecules that react with both antibodies is determined and used to
CC calculate the content of physiologically active (A). The method is used
CC for diagnosis of calcium-metabolism disorders, osteopathy, or hypo- or
CC hyper-parathyroidism. The method (unlike known assays) recognizes that
CC (i) some fragments of (A) shorter than the complete (84 aa) peptide are
CC active and (ii) that apparently intact peptide may be biologically
CC inactive, and also takes into account the fact that some fragments of (A)
CC are antagonistic (these have the receptor-binding site but lack the N-
CC terminus). It thus provides a true measure of the content of
CC physiologically active (A); contrast methods that measure intact peptide
CC and its 1-37 fragment which may produce falsely high values. This
CC sequence represents a peptide fragment used to illustrate the method of
CC the invention
XX
SQ Sequence 9 AA;

Query Match 67.2%; Score 41; DB 4; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.4e+06;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 VSEIQFMHN 10
||||| |||
Db 1 VSEIQLMHN 9

RESULT 9
AAR91645
ID AAR91645 standard; peptide; 9 AA.
XX
AC AAR91645;
XX
DT 06-NOV-1996 (first entry)
XX
DE Human parathyroid hormone antigenic peptide hPTH 1-9.
XX
KW Human parathyroid hormone; hPTH; antigen; alpha-helix; immunogen;
KW diagnosis; active hPTH 1-37.
XX
OS Synthetic.
XX
PN DE4434551-A1.
XX
PD 04-APR-1996.
XX
PF 28-SEP-1994; 94DE-04434551.
XX
PR 28-SEP-1994; 94DE-04434551.
XX
PA (FORS/) FORSSMANN W.
XX
PI Adermann K, Forssmann W, Hock D, Maegerlein M;
XX
DR WPI; 1996-180391/19.
XX
PT New antigenic peptide(s) from human parathyroid hormone - and antibodies
PT generated using them, able to distinguish between active and inactive
PT forms of the hormone.
XX
PS Claim 2; Page 4; 5pp; German.
XX
CC The present sequence is a specific example of claimed immunogenic
CC peptides having a sequence from hPTH(1-37) which includes the N- or C-
CC terminal alpha-helical region and/or the non-structured region of the
CC hormone. Antibodies and their binding fragments generated by injecting an
CC animal with the peptides are useful as diagnostic reagents for
CC determination of biologically active hPTH(1-37)
XX
SQ Sequence 9 AA;

Query Match 63.9%; Score 39; DB 2; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.4e+06;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SVSEIQFMH 9
|||||| ||
Db 1 SVSEIQLMH 9

RESULT 10
AAY96981
ID AAY96981 standard; peptide; 9 AA.
XX
AC AAY96981;
XX
DT 31-OCT-2000 (first entry)
XX
DE Parathyroid hormone N-terminal signaling domain.
XX
KW PTH; parathyroid hormone; N-terminal; signaling domain; bone mass;
KW bone reformation; resorption; remodeling; tether1; osteoporosis.
XX
OS Homo sapiens.
XX
PN WO200039278-A2.
XX
PD 06-JUL-2000.
XX
PF 30-DEC-1999; 99WO-US031108.
XX
PR 31-DEC-1998; 98US-0114577P.
XX
PA (GARD/) GARDELLA T J.
PA (KRON/) KRONENBERG H M.
PA (POTT/) POTTS J T.
PA (JUEP/) JUEPPNER H.
XX
PI Gardella TJ, Kronenberg HM, Potts JT, Jueppner H;
XX
DR WPI; 2000-452384/39.
XX
PT New compound comprising an amino terminal signaling functional domain
PT linked to a carboxy-terminal binding portion of parathyroid hormone for
PT treating mammalian conditions characterized by decreases in bone mass.
XX
PS Claim 11; Page 93; 119pp; English.
XX
CC Compounds of the structure or formula S-(L)_n-B, R_1-S-(L)_n-R or S-(L)_n
CC -R, are new. S is an amino terminal signaling functional domain of
CC parathyroid hormone (PTH); L is a linker molecule present n times (where
CC n is a positive integer 1-10 (preferably 4)); B is a C-terminal binding
CC portion of PTH(1-34) or a PTH-related protein (PTH-rP) (1-34); R_1 is the
CC PTH-1 receptor signal sequence; and R is (a portion of) PTH-1 receptor
CC sequence. The new compounds are used for treating mammalian conditions
CC characterized by decreases in bone mass, determining rates of bone
CC reformation, bone resorption and/or bone remodeling, treating diseases
CC and disorders associated with decreased tether1 activity, increasing cAMP
CC in a mammalian cell having PTH-1 receptors, or screening for a peptide or

```
CC   non-peptide PTH (claimed). The new compound can be administered by
CC   inhalation unlike the large native PTH or PTHrP which avoids the need for
CC   regular injections to treat osteoporosis
XX
SQ   Sequence 9 AA;

  Query Match             63.9%;  Score 39;  DB 3;  Length 9;
  Best Local Similarity   88.9%;  Pred. No. 1.4e+06;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 SVSEIQFMH 9
              |||||| ||
Db          1 SVSEIQLMH 9


RESULT 11
AAB86220
ID   AAB86220 standard; peptide; 9 AA.
XX
AC   AAB86220;
XX
DT   03-SEP-2001 (first entry)
XX
DE   Human parathyroid hormone immunogenic peptide SEQ ID 2.
XX
KW   Parathyroid hormone; hPTH; immunogenic peptide; human; epitope;
KW   diagnosis; calcium-metabolism disorder; osteopathy; antagonist;
KW   hypo-parathyroidism; hyper-parathyroidism.
XX
OS   Homo sapiens.
XX
PN   DE19961350-A1.
XX
PD   21-JUN-2001.
XX
PF   17-DEC-1999;   99DE-01061350.
XX
PR   17-DEC-1999;   99DE-01061350.
XX
PA   (IMMU-) IMMUNDIAGNOSTIK AG.
XX
PI   Armbruster FP;
XX
DR   WPI; 2001-376318/40.
XX
PT   Determining the content of physiologically active parathyroid hormone,
PT   useful in diagnosis of calcium-metabolism disorders, using two antibodies
PT   reactive with different epitopes.
XX
PS   Disclosure; Page 3; 10pp; German.
XX
CC   This invention describes a novel method for determining (M1) the content
CC   of active parathyroid hormone (A) by treating a sample with (i) antibody
CC   (Ab1) that recognizes the epitope formed by amino acids (aa) 1-3 of (A),
CC   and including the N-terminal residue and (ii) antibody (Ab2) that
CC   recognizes an epitope within the receptor-binding site of (A). The number
CC   of molecules that react with both antibodies is determined and used to
CC   calculate the content of physiologically active (A). The method is used
CC   for diagnosis of calcium-metabolism disorders, osteopathy, or hypo- or
CC   hyper-parathyroidism. The method (unlike known assays) recognizes that
CC   (i) some fragments of (A) shorter than the complete (84 aa) peptide are
CC   active and (ii) that apparently intact peptide may be biologically
CC   inactive, and also takes into account the fact that some fragments of (A)
CC   are antagonistic (these have the receptor-binding site but lack the N-
CC   terminus). It thus provides a true measure of the content of
CC   physiologically active (A); contrast methods that measure intact peptide
CC   and its 1-37 fragment which may produce falsely high values. This
CC   sequence represents a peptide fragment used to illustrate the method of
CC   the invention
XX
SQ   Sequence 9 AA;

  Query Match             63.9%;  Score 39;  DB 4;  Length 9;
  Best Local Similarity   88.9%;  Pred. No. 1.4e+06;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 SVSEIQFMH 9
              |||||| ||
Db          1 SVSEIQLMH 9


RESULT 12
AAY50600
ID   AAY50600 standard; peptide; 11 AA.
XX
AC   AAY50600;
XX
DT   09-FEB-2000 (first entry)
XX
DE   Resin bound cyclic peptide 33.
XX
KW   Cyclic peptide; resin bound; parathyroid hormone; osteopathic; disease;
KW   hypotensive; PTH receptor; treatment; hyper-calcemia; hypo-calcemia;
KW   osteoporosis; osteopenia; hyper-parathyroidism; hypo-parathyroidism;
KW   Cushing's syndrome; renal failure; hypertension; bone fracture repair.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 1
FT                   /note= "FMOC-Ala"
FT   Misc-difference 3
FT                   /note= "Ser(OtBu)"
FT   Misc-difference 4
FT                   /note= "Glu(OtBu)"
FT   Misc-difference 6
FT                   /note= "Gln(Trt)"
FT   Misc-difference 9
FT                   /note= "His(Trt)"
FT   Misc-difference 10
FT                   /note= "Asn(Trt)"
XX
PN   WO9952933-A1.
XX
PD   21-OCT-1999.
XX
PF   15-APR-1999;   99WO-US008435.
XX
PR   15-APR-1998;   98US-0081897P.
XX
PA   (RHON ) RHONE-POULENC RORER PHARM INC.
XX
PI   Sledeski AW,  Mencel JJ;
XX
DR   WPI; 1999-633822/54.
XX
PT   Convergent synthesis of peptides for treating e.g. bone disorders.
XX
PS   Disclosure; Page 75; 85pp; English.
XX
CC   This invention describes a novel method for the preparation of peptides
CC   (II) that contain both cyclic and linear peptide fragments comprises
CC   sequential reaction of a resin-bound linear fragment with the cyclic
CC   fragment in N-protected form and optionally other linear fragments. The
CC   products of the invention have osteopathic and hypotensive activity. (II)
CC   bind to hPTH receptors and act as agonists or antagonists of hPTH. The
CC   method is particularly used to prepare cyclic peptide analogs of
CC   parathyroid hormone (PTH) or PTH-related peptides which are useful for
CC   treating diseases that respond to treatment with agents that bind to PTH
CC   receptors (with or without activation of adenylyl cyclase activity), e.g.
CC   hyper- or hypo-calcemia, osteoporosis, osteopenia, hyper- or hypo-
CC   parathyroidism, Cushing's syndrome, renal failure and hypertension, also
CC   for promoting repair of bone fractures. Separate synthesis of the cyclic
CC   fragment allows convergent synthesis of resin-bound (II), with better
CC   yields and higher throughput. The difficulties associated with
CC   preparation of the bridged fragment are confined to a small peptide which
```

```
CC   can be purified before reaction with the resin-bound component. AAY50568-
CC   Y50614 represent the peptide fragments described in the method of the
CC   invention
XX
SQ   Sequence 11 AA;

  Query Match             63.1%;  Score 38.5;  DB 2;  Length 11;
  Best Local Similarity   75.0%;  Pred. No. 1.5;
  Matches    9;  Conservative    2;  Mismatches    0;  Indels    1;  Gaps    1;

Qy          1 SVSEIQFMHNLG 12
              :||||| :||||
Db          1 AVSEIQ-LHNLG 11


RESULT 13
AAB01862
ID   AAB01862 standard; peptide; 9 AA.
XX
AC   AAB01862;
XX
DT   11-SEP-2000  (first entry)
XX
DE   PTH(1-14)/PTHrP(1-14)-derived peptide, SEQ ID NO:6.
XX
KW   Parathyroid hormone peptide; PTH; PTH-related peptide; PTHrP;
KW   calcium homeostasis; PTH-1 receptor; PTH-2; vitamin D synthesis;
KW   bone synthesis; agonist; osteoporosis; non-parenteral delivery.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200023594-A1.
XX
PD   27-APR-2000.
XX
PF   20-OCT-1999;   99WO-US024481.
XX
PR   22-OCT-1998;   98US-0105530P.
XX
PA   (GARD/) GARDELLA T J.
PA   (KRON/) KRONENBERG H M.
PA   (POTT/) POTTS J T.
PA   (JUEP/) JUEPPNER H.
XX
PI   Gardella TJ,  Kronenberg HM,  Potts JT,  Jueppner H;
XX
DR   WPI; 2000-339693/29.
XX
PT   Parathyroid hormone (PTH) peptides, PTH related peptides and the nucleic
PT   acids that encode them, useful for treating osteoporosis.
XX
PS   Disclosure; Page 26; 73pp; English.
XX
CC   The invention relates to a novel parathyroid hormone (PTH) peptide
CC   (AAB01859) and parathyroid hormone-related peptide (PTHrP; AAB01860), and
CC   biologically active derivatives thereof (AAB01857-B01858, AAB01861-
CC   B01869). The peptides of the invention are at least 85% identical to the
CC   generic peptide of the formula: X1-Val-Ser-Glu-X2-Gln-Leu-X3-His-X4-X5-
CC   Gly-Lys-X6 (AAB01857) where: X1 is Ser or Ala; X2 is Ile or Lys; X3 is
CC   Met, Leu or Nle; X4 is Asn or Asp; X5 is Leu or Lys; X6 is His or Ser;
CC   provided that the peptide is not PTHrP(1-14). The peptides of the
CC   invention also encompass fragments of peptides of the invention
CC   consisting of amino acids 1-9, 1-10, 1-11, 1-12 and 1-13, and N- and C-
CC   terminal derivatives. PTH is a major regulator of calcium homeostasis,
CC   and is necessary for the normal function of the gastrointestinal,
CC   skeletal, neurological system, neuromuscular and cardiovascular systems.
CC   It binds to both PTH-1 receptors on osteoblasts and renal tubular cells,
CC   and to the recently identified PTH-2 receptor. PTH has a potent anabolic
CC   effect on the skeleton, and mediates calcium reabsorption, enhances
CC   phosphate clearance and vitamin D synthesis in the kidney. A homologous
CC   calls of protein hormones, the PTH-related proteins (PTHrP) mimic some of
CC   the renal and skeletal actions of PTH, and also bind to the PTH-1
CC   receptor. They do not bind to the PTH-2 receptor. The peptides of the
CC   invention are either agonists of PTH-1 and PTH-2 receptors (AAB01858,
CC   AAB01861-B01866) or are PTH-1/PTH-2 receptor antagonists (AAB01867-
CC   B01869). PTH-1/PTH-2 receptor agonists are useful for the treatment of
CC   conditions characterised by a decrease in bone mass, such as
CC   osteoporosis. PTH-1/PTH-2 receptor antagonists are useful for treating
CC   medical disorders that arise from excessive or altered action of the PTH-
CC   1/PTH-2 receptor. Detectably labelled peptides of the invention are also
CC   useful in the determination of rates of bone formation, bone resorption
CC   and/or bone remodelling in a patient. The peptides of the invention are
CC   "minimised" versions of PTH or PTHrP which are inexpensive to prepare by
CC   conventional synthetic chemistry, and can be delivered to a patient via
CC   non-parenteral routes. Sequences AAB01858 and AAB01861-B01866 represent
CC   PTH-1/PTH-2 receptor agonists
XX
SQ   Sequence 9 AA;

  Query Match             59.0%;  Score 36;  DB 3;  Length 9;
  Best Local Similarity   77.8%;  Pred. No. 1.4e+06;
  Matches    7;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 SVSEIQFMH 9
              :||||| ||
Db          1 AVSEIQLMH 9


RESULT 14
AAY96966
ID   AAY96966 standard; peptide; 9 AA.
XX
AC   AAY96966;
XX
DT   31-OCT-2000  (first entry)
XX
DE   Parathyroid hormone N-terminal signaling domain (residues 1-9).
XX
KW   PTH; parathyroid hormone; N-terminal; signaling domain; bone mass;
KW   bone reformation; resorption; remodeling; tether1; osteoporosis.
XX
OS   Homo sapiens.
XX
PN   WO200039278-A2.
XX
PD   06-JUL-2000.
XX
PF   30-DEC-1999;   99WO-US031108.
XX
PR   31-DEC-1998;   98US-0114577P.
XX
PA   (GARD/) GARDELLA T J.
PA   (KRON/) KRONENBERG H M.
PA   (POTT/) POTTS J T.
PA   (JUEP/) JUEPPNER H.
XX
PI   Gardella TJ,  Kronenberg HM,  Potts JT,  Jueppner H;
XX
DR   WPI; 2000-452384/39.
XX
PT   New compound comprising an amino terminal signaling functional domain
PT   linked to a carboxy-terminal binding portion of parathyroid hormone for
PT   treating mammalian conditions characterized by decreases in bone mass.
XX
PS   Claim 4; Page 92; 119pp; English.
XX
CC   Compounds of the structure or formula S-(L)_n-B, R_1-S-(L)_n-R or S-(L)_n
CC   -R, are new. S is an amino terminal signaling functional domain of
CC   parathyroid hormone (PTH); L is a linker molecule present n times (where
CC   n is a positive integer 1-10 (preferably 4)); B is a C-terminal binding
CC   portion of PTH(1-34) or a PTH-related protein (PTH-rP) (1-34); R_1 is the
CC   PTH-1 receptor signal sequence; and R is (a portion of) PTH-1 receptor
CC   sequence. The new compounds are used for treating mammalian conditions
CC   characterized by decreases in bone mass, determining rates of bone
CC   reformation, bone resorption and/or bone remodeling, treating diseases
```

CC and disorders associated with decreased tether1 activity, increasing cAMP
CC in a mammalian cell having PTH-1 receptors, or screening for a peptide or
CC non-peptide PTH (claimed). The new compound can be administered by
CC inhalation unlike the large native PTH or PTHrP which avoids the need for
CC regular injections to treat osteoporosis
XX
SQ Sequence 9 AA;

Query Match 59.0%; Score 36; DB 3; Length 9;
Best Local Similarity 77.8%; Pred. No. 1.4e+06;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SVSEIQFMH 9
:||||| ||
Db 1 AVSEIQLMH 9

RESULT 15
AAB01863
ID AAB01863 standard; peptide; 9 AA.
XX
AC AAB01863;
XX
DT 11-SEP-2000 (first entry)
XX
DE PTH(1-14)/PTHrP(1-14)-derived peptide, SEQ ID NO:7.
XX
KW Parathyroid hormone peptide; PTH; PTH-related peptide; PTHrP;
KW calcium homeostasis; PTH-1 receptor; PTH-2; vitamin D synthesis;
KW bone synthesis; agonist; osteoporosis; non-parenteral delivery.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200023594-A1.
XX
PD 27-APR-2000.
XX
PF 20-OCT-1999; 99WO-US024481.
XX
PR 22-OCT-1998; 98US-0105530P.
XX
PA (GARD/) GARDELLA T J.
PA (KRON/) KRONENBERG H M.
PA (POTT/) POTTS J T.
PA (JUEP/) JUEPPNER H.
XX
PI Gardella TJ, Kronenberg HM, Potts JT, Jueppner H;
XX
DR WPI; 2000-339693/29.
XX
PT Parathyroid hormone (PTH) peptides, PTH related peptides and the nucleic
PT acids that encode them, useful for treating osteoporosis.
XX
PS Disclosure; Page 26; 73pp; English.
XX
CC The invention relates to a novel parathyroid hormone (PTH) peptide
CC (AAB01859) and parathyroid hormone-related peptide (PTHrP; AAB01860), and
CC biologically active derivatives thereof (AAB01857-B01858, AAB01861-
CC B01869). The peptides of the invention are at least 85% identical to the
CC generic peptide of the formula: X1-Val-Ser-Glu-X2-Gln-Leu-X3-His-X4-X5-
CC Gly-Lys-X6 (AAB01857) where: X1 is Ser or Ala; X2 is Ile or Lys; X3 is
CC Met, Leu or Nle; X4 is Asn or Asp; X5 is Leu or Lys; X6 is His or Ser;
CC provided that the peptide is not PTHrP(1-14). The peptides of the
CC invention also encompass fragments of peptides of the invention
CC consisting of amino acids 1-9, 1-10, 1-11, 1-12 and 1-13, and N- and C-
CC terminal derivatives. PTH is a major regulator of calcium homeostasis,
CC and is necessary for the normal function of the gastrointestinal,
CC skeletal, neurological system, neuromuscular and cardiovascular systems.
CC It binds to both PTH-1 receptors on osteoblasts and renal tubular cells,
CC and to the recently identified PTH-2 receptor. PTH has a potent anabolic
CC effect on the skeleton, and mediates calcium reabsorption, enhances
CC phosphate clearance and vitamin D synthesis in the kidney. A homologous
CC calls of protein hormones, the PTH-related proteins (PTHrP) mimic some of
CC the renal and skeletal actions of PTH, and also bind to the PTH-1
CC receptor. They do not bind to the PTH-2 receptor. The peptides of the
CC invention are either agonists of PTH-1 and PTH-2 receptors (AAB01858,
CC AAB01861-B01866) or are PTH-1/PTH-2 receptor antagonists (AAB01867-
CC B01869). PTH-1/PTH-2 receptor agonists are useful for the treatment of
CC conditions characterised by a decrease in bone mass, such as
CC osteoporosis. PTH-1/PTH-2 receptor antagonists are useful for treating
CC medical disorders that arise from excessive or altered action of the PTH-
CC 1/PTH-2 receptor. Detectably labelled peptides of the invention are also
CC useful in the determination of rates of bone formation, bone resorption
CC and/or bone remodelling in a patient. The peptides of the invention are
CC "minimised" versions of PTH or PTHrP which are inexpensive to prepare by
CC conventional synthetic chemistry, and can be delivered to a patient via
CC non-parenteral routes. Sequences AAB01858 and AAB01861-B01866 represent
CC PTH-1/PTH-2 receptor agonists
XX
SQ Sequence 9 AA;

Query Match 54.1%; Score 33; DB 3; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.4e+06;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SVSEIQFMH 9
:||||| :|
Db 1 AVSEIQLLH 9

Search completed: September 5, 2004, 09:34:30
Job time : 36.5 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: September 5, 2004, 09:37:09 ; Search time 32.5 Seconds
(without alignments)
116.332 Million cell updates/sec

Title: US-09-730-174A-4
Perfect score: 61
Sequence: 1 SVSEIQFMHNLG 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1298764 seqs, 315065143 residues

Total number of hits satisfying chosen parameters: 182187

Minimum DB seq length: 0
Maximum DB seq length: 12

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	61	100.0	12	9	US-09-730-174A-4	Sequence 4, Appli
2	58	95.1	12	9	US-09-730-174A-6	Sequence 6, Appli
3	57	93.4	11	9	US-09-730-174A-2	Sequence 2, Appli
4	55	90.2	12	9	US-09-730-174A-3	Sequence 3, Appli
5	52	85.2	12	9	US-09-730-174A-5	Sequence 5, Appli
6	51	83.6	11	9	US-09-730-174A-1	Sequence 1, Appli
7	45	73.8	10	14	US-10-168-185-1	Sequence 1, Appli
8	41	67.2	9	14	US-10-168-185-7	Sequence 7, Appli
9	39	63.9	9	14	US-10-168-185-2	Sequence 2, Appli
10	37	60.7	8	14	US-10-168-185-8	Sequence 8, Appli
11	36	59.0	9	14	US-10-192-673-6	Sequence 6, Appli
12	33	54.1	9	14	US-10-192-673-7	Sequence 7, Appli
13	31	50.8	8	14	US-10-168-185-3	Sequence 3, Appli
14	29	47.5	9	14	US-10-192-673-10	Sequence 10, Appl
15	27	44.3	10	14	US-10-033-741-61	Sequence 61, Appl
16	26	42.6	6	14	US-10-168-185-5	Sequence 5, Appli
17	26	42.6	7	14	US-10-168-185-4	Sequence 4, Appli
18	26	42.6	9	14	US-10-192-673-8	Sequence 8, Appli
19	26	42.6	10	14	US-10-168-185-11	Sequence 11, Appl
20	25	41.0	10	15	US-10-137-867-526	Sequence 526, App
21	25	41.0	10	15	US-10-366-709-2	Sequence 2, Appli
22	24	39.3	9	9	US-09-834-765-45	Sequence 45, Appl
23	24	39.3	9	9	US-09-834-765-55	Sequence 55, Appl
24	24	39.3	9	9	US-09-746-945-6	Sequence 6, Appli
25	24	39.3	10	9	US-09-834-765-73	Sequence 73, Appl
26	24	39.3	10	9	US-09-834-765-78	Sequence 78, Appl
27	24	39.3	10	14	US-10-232-187-8	Sequence 8, Appli
28	24	39.3	11	14	US-10-153-334-14	Sequence 14, Appl
29	24	39.3	11	16	US-10-391-364-93	Sequence 93, Appl
30	24	39.3	12	14	US-10-319-130-16	Sequence 16, Appl
31	23	37.7	8	14	US-10-043-487-508	Sequence 508, App
32	23	37.7	9	14	US-10-147-140-26	Sequence 26, Appl
33	23	37.7	9	15	US-10-024-652-120	Sequence 120, App
34	23	37.7	9	15	US-10-024-652-339	Sequence 339, App
35	23	37.7	9	15	US-10-024-652-407	Sequence 407, App
36	23	37.7	9	15	US-10-024-652-956	Sequence 956, App
37	23	37.7	9	15	US-10-024-652-1094	Sequence 1094, Ap
38	23	37.7	9	15	US-10-024-652-1259	Sequence 1259, Ap
39	23	37.7	9	15	US-10-024-652-1385	Sequence 1385, Ap
40	23	37.7	9	15	US-10-024-652-1464	Sequence 1464, Ap
41	23	37.7	9	15	US-10-024-652-2057	Sequence 2057, Ap
42	23	37.7	9	15	US-10-024-652-2058	Sequence 2058, Ap
43	23	37.7	10	9	US-09-976-787-4	Sequence 4, Appli
44	23	37.7	10	9	US-09-865-198-4	Sequence 4, Appli
45	23	37.7	10	9	US-09-965-099-12	Sequence 12, Appl

ALIGNMENTS

RESULT 1
US-09-730-174A-4
; Sequence 4, Application US/09730174A
; Patent No. US20020110871A1
; GENERAL INFORMATION:
; APPLICANT: Zahradnik, R.J.
; TITLE OF INVENTION: Antibodies and Peptide Antigens for Producing Antibodies having
; TITLE OF INVENTION: Selective Binding Specificity to Bioactive Intact Parathyroid H
; FILE REFERENCE: IMUNE-001A
; CURRENT APPLICATION NUMBER: US/09/730,174A
; CURRENT FILING DATE: 2000-12-05
; NUMBER OF SEQ ID NOS: 12
; SEQ ID NO 4
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Induces Formation of Antibodies and Isolates said Antibodies
US-09-730-174A-4

Query Match 100.0%; Score 61; DB 9; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.00015;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQFMHNLG 12
||||||||||||
Db 1 SVSEIQFMHNLG 12

RESULT 2
US-09-730-174A-6
; Sequence 6, Application US/09730174A
; Patent No. US20020110871A1
; GENERAL INFORMATION:
; APPLICANT: Zahradnik, R.J.
; TITLE OF INVENTION: Antibodies and Peptide Antigens for Producing Antibodies having
; TITLE OF INVENTION: Selective Binding Specificity to Bioactive Intact Parathyroid H
; FILE REFERENCE: IMUNE-001A

; CURRENT APPLICATION NUMBER: US/09/730,174A
; CURRENT FILING DATE: 2000-12-05
; NUMBER OF SEQ ID NOS: 12
; SEQ ID NO 6
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Induces Formation of Antibodies and Isolates said Antibodies
US-09-730-174A-6

Query Match 95.1%; Score 58; DB 9; Length 12;
Best Local Similarity 91.7%; Pred. No. 0.00054;
Matches 11; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQFMHNLG 12
:||||||||||||
Db 1 AVSEIQFMHNLG 12

RESULT 3
US-09-730-174A-2
; Sequence 2, Application US/09730174A
; Patent No. US20020110871A1
; GENERAL INFORMATION:
; APPLICANT: Zahradnik, R.J.
; TITLE OF INVENTION: Antibodies and Peptide Antigens for Producing Antibodies having a
; TITLE OF INVENTION: Selective Binding Specificity to Bioactive Intact Parathyroid Ho
; FILE REFERENCE: IMUNE-001A
; CURRENT APPLICATION NUMBER: US/09/730,174A
; CURRENT FILING DATE: 2000-12-05
; NUMBER OF SEQ ID NOS: 12
; SEQ ID NO 2
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Induces Formation of Antibodies and Isolates said Antibodies
US-09-730-174A-2

Query Match 93.4%; Score 57; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.00075;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VSEIQFMHNLG 12
||||||||||||
Db 1 VSEIQFMHNLG 11

RESULT 4
US-09-730-174A-3
; Sequence 3, Application US/09730174A
; Patent No. US20020110871A1
; GENERAL INFORMATION:
; APPLICANT: Zahradnik, R.J.
; TITLE OF INVENTION: Antibodies and Peptide Antigens for Producing Antibodies having a
; TITLE OF INVENTION: Selective Binding Specificity to Bioactive Intact Parathyroid Ho
; FILE REFERENCE: IMUNE-001A
; CURRENT APPLICATION NUMBER: US/09/730,174A
; CURRENT FILING DATE: 2000-12-05
; NUMBER OF SEQ ID NOS: 12
; SEQ ID NO 3
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Induces Formation of Antibodies and Isolates said Antibodies
US-09-730-174A-3

Query Match 90.2%; Score 55; DB 9; Length 12;
Best Local Similarity 91.7%; Pred. No. 0.0019;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SVSEIQFMHNLG 12
|||||| |||||
Db 1 SVSEIQLMHNLG 12

RESULT 5
US-09-730-174A-5
; Sequence 5, Application US/09730174A
; Patent No. US20020110871A1
; GENERAL INFORMATION:
; APPLICANT: Zahradnik, R.J.
; TITLE OF INVENTION: Antibodies and Peptide Antigens for Producing Antibodies having a
; TITLE OF INVENTION: Selective Binding Specificity to Bioactive Intact Parathyroid Ho
; FILE REFERENCE: IMUNE-001A
; CURRENT APPLICATION NUMBER: US/09/730,174A
; CURRENT FILING DATE: 2000-12-05
; NUMBER OF SEQ ID NOS: 12
; SEQ ID NO 5
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Induces Formation of Antibodies and Isolates said Antibodies
US-09-730-174A-5

Query Match 85.2%; Score 52; DB 9; Length 12;
Best Local Similarity 83.3%; Pred. No. 0.0069;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SVSEIQFMHNLG 12
:||||| |||||
Db 1 AVSEIQLMHNLG 12

RESULT 6
US-09-730-174A-1
; Sequence 1, Application US/09730174A
; Patent No. US20020110871A1
; GENERAL INFORMATION:
; APPLICANT: Zahradnik, R.J.
; TITLE OF INVENTION: Antibodies and Peptide Antigens for Producing Antibodies having a
; TITLE OF INVENTION: Selective Binding Specificity to Bioactive Intact Parathyroid Ho
; FILE REFERENCE: IMUNE-001A
; CURRENT APPLICATION NUMBER: US/09/730,174A
; CURRENT FILING DATE: 2000-12-05
; NUMBER OF SEQ ID NOS: 12
; SEQ ID NO 1
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Induces Formation of Antibodies and Isolates said Antibodies
US-09-730-174A-1

Query Match 83.6%; Score 51; DB 9; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.0097;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 VSEIQFMHNLG 12
||||| |||||
Db 1 VSEIQLMHNLG 11

RESULT 7
US-10-168-185-1
; Sequence 1, Application US/10168185
; Publication No. US20030175802A1
; GENERAL INFORMATION:
; APPLICANT: Armbruster, Franz Paul
; APPLICANT: Missbichler, Albert
; APPLICANT: Schmidt-Gayk, Heinrich
; APPLICANT: Roth, Heinz-Jurgen
; TITLE OF INVENTION: Method for Determining Parathormone

; TITLE OF INVENTION: Activity in a Human Sample
; FILE REFERENCE: HLZ-004US
; CURRENT APPLICATION NUMBER: US/10/168,185
; CURRENT FILING DATE: 2002-06-17
; PRIOR APPLICATION NUMBER: PCT/EP00/12911
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: DE 19961350
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-168-185-1

Query Match 73.8%; Score 45; DB 14; Length 10;
Best Local Similarity 90.0%; Pred. No. 0.11;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SVSEIQFMHN 10
||||||.|||
Db 1 SVSEIQLMHN 10

RESULT 8
US-10-168-185-7
; Sequence 7, Application US/10168185
; Publication No. US20030175802A1
; GENERAL INFORMATION:
; APPLICANT: Armbruster, Franz Paul
; APPLICANT: Missbichler, Albert
; APPLICANT: Schmidt-Gayk, Heinrich
; APPLICANT: Roth, Heinz-Jurgen
; TITLE OF INVENTION: Method for Determining Parathormone
; TITLE OF INVENTION: Activity in a Human Sample
; FILE REFERENCE: HLZ-004US
; CURRENT APPLICATION NUMBER: US/10/168,185
; CURRENT FILING DATE: 2002-06-17
; PRIOR APPLICATION NUMBER: PCT/EP00/12911
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: DE 19961350
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-168-185-7

Query Match 67.2%; Score 41; DB 14; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.2e+06;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 VSEIQFMHN 10
|||||.|||
Db 1 VSEIQLMHN 9

RESULT 9
US-10-168-185-2
; Sequence 2, Application US/10168185
; Publication No. US20030175802A1
; GENERAL INFORMATION:
; APPLICANT: Armbruster, Franz Paul
; APPLICANT: Missbichler, Albert
; APPLICANT: Schmidt-Gayk, Heinrich
; APPLICANT: Roth, Heinz-Jurgen
; TITLE OF INVENTION: Method for Determining Parathormone
; TITLE OF INVENTION: Activity in a Human Sample
; FILE REFERENCE: HLZ-004US
; CURRENT APPLICATION NUMBER: US/10/168,185
; CURRENT FILING DATE: 2002-06-17
; PRIOR APPLICATION NUMBER: PCT/EP00/12911
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: DE 19961350
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-168-185-2

Query Match 63.9%; Score 39; DB 14; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.2e+06;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SVSEIQFMH 9
||||||.||
Db 1 SVSEIQLMH 9

RESULT 10
US-10-168-185-8
; Sequence 8, Application US/10168185
; Publication No. US20030175802A1
; GENERAL INFORMATION:
; APPLICANT: Armbruster, Franz Paul
; APPLICANT: Missbichler, Albert
; APPLICANT: Schmidt-Gayk, Heinrich
; APPLICANT: Roth, Heinz-Jurgen
; TITLE OF INVENTION: Method for Determining Parathormone
; TITLE OF INVENTION: Activity in a Human Sample
; FILE REFERENCE: HLZ-004US
; CURRENT APPLICATION NUMBER: US/10/168,185
; CURRENT FILING DATE: 2002-06-17
; PRIOR APPLICATION NUMBER: PCT/EP00/12911
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: DE 19961350
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-168-185-8

Query Match 60.7%; Score 37; DB 14; Length 8;
Best Local Similarity 87.5%; Pred. No. 1.2e+06;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 SEIQFMHN 10
||||.|||
Db 1 SEIQLMHN 8

RESULT 11
US-10-192-673-6
; Sequence 6, Application US/10192673
; Publication No. US20030166838A1
; GENERAL INFORMATION:
; APPLICANT: Gardella, Thomas J.
; APPLICANT: Kronenberg, Henry
; APPLICANT: Potts, John T.
; APPLICANT: Juppner, Harald
; TITLE OF INVENTION: Bioactive Peptides and Peptide Derivatives of
; TITLE OF INVENTION: Parathyroid Hormone (PTH) and Parathyroid
; TITLE OF INVENTION: Hormone-Related Peptide (PTHrP)
; FILE REFERENCE: 0609.4570002
; CURRENT APPLICATION NUMBER: US/10/192,673
; CURRENT FILING DATE: 2002-07-11
; PRIOR APPLICATION NUMBER: U.S. 09/421,379

```
;  PRIOR FILING DATE: 1999-10-20
;  PRIOR APPLICATION NUMBER: U.S. 60/105,530
;  PRIOR FILING DATE: 1998-10-22
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
;    LENGTH: 9
;    TYPE: PRT
;    ORGANISM: Artificial Sequence
;    FEATURE:
;    OTHER INFORMATION: Description of Artificial Sequence: synthetic
;    OTHER INFORMATION: peptide
US-10-192-673-6

  Query Match             59.0%;  Score 36;  DB 14;  Length 9;
  Best Local Similarity   77.8%;  Pred. No. 1.2e+06;
  Matches    7;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 SVSEIQFMH 9
              :|||||  ||
Db          1 AVSEIQLMH 9


RESULT 12
US-10-192-673-7
; Sequence 7, Application US/10192673
; Publication No. US20030166838A1
; GENERAL INFORMATION:
;  APPLICANT: Gardella, Thomas J.
;  APPLICANT:  Kronenberg, Henry
;  APPLICANT:  Potts, John T.
;  APPLICANT:  Juppner, Harald
;  TITLE OF INVENTION: Bioactive Peptides and Peptide Derivatives of
;  TITLE OF INVENTION:  Parathyroid Hormone (PTH) and Parathyroid
;  TITLE OF INVENTION:  Hormone-Related Peptide (PTHrP)
;  FILE REFERENCE: 0609.4570002
;  CURRENT APPLICATION NUMBER: US/10/192,673
;  CURRENT FILING DATE:  2002-07-11
;  PRIOR APPLICATION NUMBER: U.S. 09/421,379
;  PRIOR FILING DATE: 1999-10-20
;  PRIOR APPLICATION NUMBER: U.S. 60/105,530
;  PRIOR FILING DATE: 1998-10-22
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
;    LENGTH: 9
;    TYPE: PRT
;    ORGANISM: Artificial Sequence
;    FEATURE:
;    OTHER INFORMATION: Description of Artificial Sequence: synthetic
;    OTHER INFORMATION: peptide
US-10-192-673-7

  Query Match             54.1%;  Score 33;  DB 14;  Length 9;
  Best Local Similarity   66.7%;  Pred. No. 1.2e+06;
  Matches    6;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 SVSEIQFMH 9
              :|||||  :|
Db          1 AVSEIQLLH 9


RESULT 13
US-10-168-185-3
; Sequence 3, Application US/10168185
; Publication No. US20030175802A1
; GENERAL INFORMATION:
;  APPLICANT: Armbruster, Franz Paul
;  APPLICANT:  Missbichler, Albert
;  APPLICANT:  Schmidt-Gayk, Heinrich
;  APPLICANT:  Roth, Heinz-Jurgen
;  TITLE OF INVENTION: Method for Determining Parathormone
;  TITLE OF INVENTION:  Activity in a Human Sample
;  FILE REFERENCE: HLZ-004US
;  CURRENT APPLICATION NUMBER: US/10/168,185
;  CURRENT FILING DATE:  2002-06-17
;  PRIOR APPLICATION NUMBER: PCT/EP00/12911
;  PRIOR FILING DATE: 2000-12-18
;  PRIOR APPLICATION NUMBER: DE 19961350
;  PRIOR FILING DATE: 1999-12-17
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;    LENGTH: 8
;    TYPE: PRT
;    ORGANISM: Homo sapiens
US-10-168-185-3

  Query Match             50.8%;  Score 31;  DB 14;  Length 8;
  Best Local Similarity   87.5%;  Pred. No. 1.2e+06;
  Matches    7;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 SVSEIQFM 8
              ||||||  |
Db          1 SVSEIQLM 8


RESULT 14
US-10-192-673-10
; Sequence 10, Application US/10192673
; Publication No. US20030166838A1
; GENERAL INFORMATION:
;  APPLICANT: Gardella, Thomas J.
;  APPLICANT:  Kronenberg, Henry
;  APPLICANT:  Potts, John T.
;  APPLICANT:  Juppner, Harald
;  TITLE OF INVENTION: Bioactive Peptides and Peptide Derivatives of
;  TITLE OF INVENTION:  Parathyroid Hormone (PTH) and Parathyroid
;  TITLE OF INVENTION:  Hormone-Related Peptide (PTHrP)
;  FILE REFERENCE: 0609.4570002
;  CURRENT APPLICATION NUMBER: US/10/192,673
;  CURRENT FILING DATE:  2002-07-11
;  PRIOR APPLICATION NUMBER: U.S. 09/421,379
;  PRIOR FILING DATE: 1999-10-20
;  PRIOR APPLICATION NUMBER: U.S. 60/105,530
;  PRIOR FILING DATE: 1998-10-22
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
;    LENGTH: 9
;    TYPE: PRT
;    ORGANISM: Artificial Sequence
;    FEATURE:
;    OTHER INFORMATION: Description of Artificial Sequence: synthetic
;    OTHER INFORMATION: peptide
US-10-192-673-10

  Query Match             47.5%;  Score 29;  DB 14;  Length 9;
  Best Local Similarity   66.7%;  Pred. No. 1.2e+06;
  Matches    6;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 SVSEIQFMH 9
              ||||  |  :|
Db          1 SVSEHQLLH 9


RESULT 15
US-10-033-741-61
; Sequence 61, Application US/10033741
; Publication No. US20030049640A1
; GENERAL INFORMATION:
;  APPLICANT: Herman, et al.
;  TITLE OF INVENTION: Proteins, Genes and Their Use For Diagnosis and Treatment of Vasc
;  TITLE OF INVENTION:  Response
;  FILE REFERENCE: 9195-079
;  CURRENT APPLICATION NUMBER: US/10/033,741
```

```
;  CURRENT FILING DATE:  2001-12-27
;  NUMBER OF SEQ ID NOS: 80
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 61
;   LENGTH: 10
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-033-741-61

  Query Match           44.3%;  Score 27;  DB 14;  Length 10;
  Best Local Similarity  55.6%;  Pred. No. 2.4e+02;
  Matches    5;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 SVSEIQFMH 9
              ||||:  :|
Db          1 SVSELPIVH 9


Search completed: September  5, 2004, 09:49:38
Job time : 33.5 secs
```

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: September 5, 2004, 09:32:03 ; Search time 11 Seconds
(without alignments)
56.319 Million cell updates/sec

Title: US-09-730-174A-4
Perfect score: 61
Sequence: 1 SVSEIQFMHNLG 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 121490

Minimum DB seq length: 0
Maximum DB seq length: 12

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	46	75.4	12	4	US-09-442-989-31	Sequence 31, Appl
2	45	73.8	10	3	US-08-817-547A-1	Sequence 1, Appli
3	39	63.9	9	3	US-08-817-547A-2	Sequence 2, Appli
4	36	59.0	9	4	US-09-421-379-6	Sequence 6, Appli
5	33	54.1	9	4	US-09-421-379-7	Sequence 7, Appli
6	31	50.8	8	3	US-08-817-547A-3	Sequence 3, Appli
7	29	47.5	9	4	US-09-421-379-10	Sequence 10, Appl
8	29	47.5	12	2	US-08-140-137A-42	Sequence 42, Appl
9	28	45.9	11	6	5460978-3	Patent No. 5460978
10	26	42.6	6	3	US-08-817-547A-5	Sequence 5, Appli
11	26	42.6	7	3	US-08-817-547A-4	Sequence 4, Appli
12	26	42.6	9	4	US-09-421-379-8	Sequence 8, Appli
13	25	41.0	12	2	US-08-482-228-42	Sequence 42, Appl
14	25	41.0	12	3	US-08-482-528-42	Sequence 42, Appl
15	24	39.3	5	2	US-08-177-109A-56	Sequence 56, Appl
16	24	39.3	5	2	US-08-687-706-56	Sequence 56, Appl
17	24	39.3	5	3	US-08-817-547A-17	Sequence 17, Appl
18	24	39.3	6	3	US-08-817-547A-16	Sequence 16, Appl
19	24	39.3	7	3	US-08-817-547A-15	Sequence 15, Appl
20	24	39.3	8	2	US-08-748-021-64	Sequence 64, Appl
21	24	39.3	8	3	US-08-817-547A-14	Sequence 14, Appl
22	24	39.3	8	3	US-08-974-297-64	Sequence 64, Appl
23	24	39.3	9	3	US-08-817-547A-13	Sequence 13, Appl
24	24	39.3	10	3	US-08-817-547A-7	Sequence 7, Appli
25	23	37.7	9	1	US-07-822-043-26	Sequence 26, Appl
26	23	37.7	9	1	US-08-346-455B-26	Sequence 26, Appl
27	23	37.7	9	3	US-08-977-221-26	Sequence 26, Appl
28	23	37.7	9	4	US-09-483-831B-26	Sequence 26, Appl
29	23	37.7	9	5	PCT-US95-06613-26	Sequence 26, Appl
30	23	37.7	10	2	US-08-116-778E-9	Sequence 9, Appli
31	23	37.7	10	2	US-08-438-562-9	Sequence 9, Appli
32	23	37.7	10	2	US-08-483-528B-97	Sequence 97, Appl
33	23	37.7	10	3	US-08-783-853A-12	Sequence 12, Appl
34	23	37.7	10	3	US-08-836-561-49	Sequence 49, Appl
35	23	37.7	10	3	US-09-280-028-12	Sequence 12, Appl
36	23	37.7	10	4	US-09-344-050-12	Sequence 12, Appl
37	23	37.7	10	4	US-09-393-385B-108	Sequence 108, App
38	23	37.7	10	4	US-09-434-122-49	Sequence 49, Appl
39	23	37.7	10	4	US-09-091-071-3	Sequence 3, Appli
40	23	37.7	11	4	US-09-556-605-61	Sequence 61, Appl
41	23	37.7	12	3	US-09-064-750-1	Sequence 1, Appli
42	23	37.7	12	4	US-09-556-605-60	Sequence 60, Appl
43	22	36.1	10	1	US-08-615-181-83	Sequence 83, Appl
44	22	36.1	10	1	US-08-555-579-2	Sequence 2, Appli
45	22	36.1	10	2	US-08-428-257A-14	Sequence 14, Appl

ALIGNMENTS

```
RESULT 1
US-09-442-989-31
; Sequence 31, Application US/09442989
; Patent No. 6569993
; GENERAL INFORMATION:
;  APPLICANT: Sledeski, Adam W.
;  APPLICANT: Mencel, James J.
;  TITLE OF INVENTION: PROCESS FOR THE PREPARATION OF RESIN-BOUND CYCLIC
;  TITLE OF INVENTION: PEPTIDES
;  FILE REFERENCE: A3113B-US
;  CURRENT APPLICATION NUMBER: US/09/442,989
;  CURRENT FILING DATE: 1999-11-18
;  EARLIER APPLICATION NUMBER: 60/081,897
;  EARLIER FILING DATE: 1998-04-15
;  NUMBER OF SEQ ID NOS: 46
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 31
;   LENGTH: 12
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: PEPTIDE
;   LOCATION: (1)
;   OTHER INFORMATION: FMOC-Ala
;   FEATURE:
;   NAME/KEY: PEPTIDE
;   LOCATION: (3)
;   OTHER INFORMATION: Ser(OtBu)
;   FEATURE:
;   NAME/KEY: PEPTIDE
;   LOCATION: (4)
;   OTHER INFORMATION: Glu(OtBu)
;   FEATURE:
;   NAME/KEY: PEPTIDE
;   LOCATION: (6)
;   OTHER INFORMATION: Gln(Trt)
;   FEATURE:
;   NAME/KEY: PEPTIDE
;   LOCATION: (9)
;   OTHER INFORMATION: His(Trt)
;   FEATURE:
;   NAME/KEY: PEPTIDE
;   LOCATION: (10)
;   OTHER INFORMATION: Asn(Trt)
;   FEATURE:
;   NAME/KEY: MOD_RES
;   LOCATION: (8)
;   OTHER INFORMATION: Nle
US-09-442-989-31
```

```
  Query Match             75.4%;  Score 46;  DB 4;  Length 12;
  Best Local Similarity   75.0%;  Pred. No. 0.013;
  Matches    9;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 SVSEIQFMHNLG 12
              :|||||  ||||
Db          1 AVSEIQLXHNLG 12


RESULT 2
US-08-817-547A-1
; Sequence 1, Application US/08817547A
; Patent No. 6030790
;  GENERAL INFORMATION:
;    APPLICANT:  Adermann, Knut
;    APPLICANT:  Hock, Dieter
;    APPLICANT:  Magerlein, Markus
;    TITLE OF INVENTION:  Peptides from the hPTH Sequence
;    NUMBER OF SEQUENCES:  36
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Jones & Askew, LLP
;      STREET:  191 Peachtree Street, 37th Floor
;      CITY:  Atlanta
;      STATE:  Georgia
;      COUNTRY:  USA
;      ZIP:  30303
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/817,547A
;      FILING DATE:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/EP95/03757
;      FILING DATE:  29 SEPT 1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  FROST, ROGER T.
;      REGISTRATION NUMBER:  22,176
;      REFERENCE/DOCKET NUMBER:  07826-0007
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  404-818-3700
;      TELEFAX:  404-818-3799
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  unknown
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  peptide
;    HYPOTHETICAL:  no
;    ANTI-SENSE:  no
US-08-817-547A-1

  Query Match             73.8%;  Score 45;  DB 3;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 0.017;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 SVSEIQFMHN 10
              ||||||  |||
Db          1 SVSEIQLMHN 10


RESULT 3
US-08-817-547A-2
; Sequence 2, Application US/08817547A
; Patent No. 6030790
;  GENERAL INFORMATION:
;    APPLICANT:  Adermann, Knut
;    APPLICANT:  Hock, Dieter
;    APPLICANT:  Magerlein, Markus
;    TITLE OF INVENTION:  Peptides from the hPTH Sequence
;    NUMBER OF SEQUENCES:  36
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Jones & Askew, LLP
;      STREET:  191 Peachtree Street, 37th Floor
;      CITY:  Atlanta
;      STATE:  Georgia
;      COUNTRY:  USA
;      ZIP:  30303
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/817,547A
;      FILING DATE:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/EP95/03757
;      FILING DATE:  29 SEPT 1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  FROST, ROGER T.
;      REGISTRATION NUMBER:  22,176
;      REFERENCE/DOCKET NUMBER:  07826-0007
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  404-818-3700
;      TELEFAX:  404-818-3799
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  9 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  unknown
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  peptide
;    HYPOTHETICAL:  no
;    ANTI-SENSE:  no
US-08-817-547A-2

  Query Match             63.9%;  Score 39;  DB 3;  Length 9;
  Best Local Similarity   88.9%;  Pred. No. 3e+05;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 SVSEIQFMH 9
              |||||| ||
Db          1 SVSEIQLMH 9


RESULT 4
US-09-421-379-6
; Sequence 6, Application US/09421379
; Patent No. 6495662
; GENERAL INFORMATION:
;  APPLICANT: Gardella, Thomas J.
;  APPLICANT: Kronenberg, Henry
;  APPLICANT: Potts, John T.
;  APPLICANT: Juppner, Harald
;  TITLE OF INVENTION: Bioactive Peptides and Peptide Derivatives of
;  TITLE OF INVENTION: Parathyroid Hormone (PTH) and Parathyroid
;  TITLE OF INVENTION: Hormone-Related Peptide (PTHrP)
;  FILE REFERENCE: 0609.4570001
;  CURRENT APPLICATION NUMBER: US/09/421,379
;  CURRENT FILING DATE: 1999-10-20
;  EARLIER APPLICATION NUMBER: U.S. 60/105,530
;  EARLIER FILING DATE: 1998-10-22
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: synthetic
;   OTHER INFORMATION: peptide
US-09-421-379-6
```

```
  Query Match           59.0%;  Score 36;  DB 4;  Length 9;
  Best Local Similarity  77.8%;  Pred. No. 3e+05;
  Matches    7;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 SVSEIQFMH 9
              :|||||  ||
Db          1 AVSEIQLMH 9


RESULT 5
US-09-421-379-7
; Sequence 7, Application US/09421379
; Patent No. 6495662
; GENERAL INFORMATION:
;  APPLICANT: Gardella, Thomas J.
;  APPLICANT: Kronenberg, Henry
;  APPLICANT: Potts, John T.
;  APPLICANT: Juppner, Harald
;  TITLE OF INVENTION: Bioactive Peptides and Peptide Derivatives of
;  TITLE OF INVENTION: Parathyroid Hormone (PTH) and Parathyroid
;  TITLE OF INVENTION: Hormone-Related Peptide (PTHrP)
;  FILE REFERENCE: 0609.4570001
;  CURRENT APPLICATION NUMBER: US/09/421,379
;  CURRENT FILING DATE: 1999-10-20
;  EARLIER APPLICATION NUMBER: U.S. 60/105,530
;  EARLIER FILING DATE: 1998-10-22
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: synthetic
;   OTHER INFORMATION: peptide
US-09-421-379-7

  Query Match           54.1%;  Score 33;  DB 4;  Length 9;
  Best Local Similarity  66.7%;  Pred. No. 3e+05;
  Matches    6;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 SVSEIQFMH 9
              :|||||  :|
Db          1 AVSEIQLLH 9


RESULT 6
US-08-817-547A-3
; Sequence 3, Application US/08817547A
; Patent No. 6030790
;  GENERAL INFORMATION:
;    APPLICANT:  Adermann, Knut
;    APPLICANT:  Hock, Dieter
;    APPLICANT:  Magerlein, Markus
;    TITLE OF INVENTION:  Peptides from the hPTH Sequence
;    NUMBER OF SEQUENCES:  36
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Jones & Askew, LLP
;      STREET:  191 Peachtree Street, 37th Floor
;      CITY:  Atlanta
;      STATE:  Georgia
;      COUNTRY:  USA
;      ZIP:  30303
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/817,547A
;      FILING DATE:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/EP95/03757
;      FILING DATE:  29 SEPT 1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  FROST, ROGER T.
;      REGISTRATION NUMBER:  22,176
;      REFERENCE/DOCKET NUMBER:  07826-0007
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  404-818-3700
;      TELEFAX:  404-818-3799
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  8 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  unknown
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  peptide
;    HYPOTHETICAL:  no
;    ANTI-SENSE:  no
US-08-817-547A-3

  Query Match           50.8%;  Score 31;  DB 3;  Length 8;
  Best Local Similarity  87.5%;  Pred. No. 3e+05;
  Matches    7;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 SVSEIQFM 8
              ||||||  |
Db          1 SVSEIQLM 8


RESULT 7
US-09-421-379-10
; Sequence 10, Application US/09421379
; Patent No. 6495662
; GENERAL INFORMATION:
;  APPLICANT: Gardella, Thomas J.
;  APPLICANT: Kronenberg, Henry
;  APPLICANT: Potts, John T.
;  APPLICANT: Juppner, Harald
;  TITLE OF INVENTION: Bioactive Peptides and Peptide Derivatives of
;  TITLE OF INVENTION: Parathyroid Hormone (PTH) and Parathyroid
;  TITLE OF INVENTION: Hormone-Related Peptide (PTHrP)
;  FILE REFERENCE: 0609.4570001
;  CURRENT APPLICATION NUMBER: US/09/421,379
;  CURRENT FILING DATE: 1999-10-20
;  EARLIER APPLICATION NUMBER: U.S. 60/105,530
;  EARLIER FILING DATE: 1998-10-22
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: synthetic
;   OTHER INFORMATION: peptide
US-09-421-379-10

  Query Match           47.5%;  Score 29;  DB 4;  Length 9;
  Best Local Similarity  66.7%;  Pred. No. 3e+05;
  Matches    6;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 SVSEIQFMH 9
              ||||  |  :|
Db          1 SVSEHQLLH 9


RESULT 8
US-08-140-137A-42
; Sequence 42, Application US/08140137A
; Patent No. 5817617
;  GENERAL INFORMATION:
;    APPLICANT:  TUOMANEN, ELAINE
;    APPLICANT:  MASURE, H. R.
```

```
;    TITLE OF INVENTION:  ANALOGS OF ENDOTHELIAL LEUKOCYTE
;    TITLE OF INVENTION:  ADHESION MOLECULE (ELAM)
;    NUMBER OF SEQUENCES:  49
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Klauber & Jackson
;      STREET:  411 Hackensack Avenue
;      CITY:  Hackensack
;      STATE:  New Jersey
;      COUNTRY:  USA
;      ZIP:  07601
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/140,137A
;      FILING DATE:  27-MAY-1994
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Jackson Esq., David A.
;      REGISTRATION NUMBER:  26,742
;      REFERENCE/DOCKET NUMBER:  600-1-096
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  201 487-5800
;      TELEFAX:  201 343-1684
;      TELEX:  133521
;  INFORMATION FOR SEQ ID NO:  42:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  12 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;      DESCRIPTION:  CaRD peptide seqence
US-08-140-137A-42

  Query Match             47.5%;  Score 29;  DB 2;  Length 12;
  Best Local Similarity   62.5%;  Pred. No. 23;
  Matches    5;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 VSEIQFMH 9
              :|| ||:|
Db          5 ISEEQFVH 12


RESULT 9
5460978-3
;Patent No. 5460978
;    APPLICANT: MARTIN, THOMAS J.;MOSELEY, JANE M.;KEMP,
;BRUCE E.;WETTENHALL, RICHARD E.H.
;    TITLE OF INVENTION: PROTEIN ACTIVE IN HUMORAL
;HYPERCALCEMIA OF MALIGNANCY-PTHRP
;    NUMBER OF SEQUENCES: 4
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/715,280
;      FILING DATE: 14-JUN-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER: 199,235
;      FILING DATE: 09-MAY-1988
;      APPLICATION NUMBER:
;      FILING DATE:
;SEQ ID NO:3:
;      LENGTH: 11
5460978-3

  Query Match             45.9%;  Score 28;  DB 6;  Length 11;
  Best Local Similarity   60.0%;  Pred. No. 32;
  Matches    6;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 SVSEIQFMHN 10
              :||| |  ||
Db          1 AVSEHQLEHN 10


RESULT 10
US-08-817-547A-5
; Sequence 5, Application US/08817547A
; Patent No. 6030790
;  GENERAL INFORMATION:
;    APPLICANT:  Adermann, Knut
;    APPLICANT:  Hock, Dieter
;    APPLICANT:  Magerlein, Markus
;    TITLE OF INVENTION:  Peptides from the hPTH Sequence
;    NUMBER OF SEQUENCES:  36
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Jones & Askew, LLP
;      STREET:  191 Peachtree Street, 37th Floor
;      CITY:  Atlanta
;      STATE:  Georgia
;      COUNTRY:  USA
;      ZIP:  30303
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/817,547A
;      FILING DATE:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/EP95/03757
;      FILING DATE:  29 SEPT 1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  FROST, ROGER T.
;      REGISTRATION NUMBER:  22,176
;      REFERENCE/DOCKET NUMBER:  07826-0007
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  404-818-3700
;      TELEFAX:  404-818-3799
;  INFORMATION FOR SEQ ID NO:  5:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  6 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  unknown
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  peptide
;    HYPOTHETICAL:  no
;    ANTI-SENSE:  no
US-08-817-547A-5

  Query Match             42.6%;  Score 26;  DB 3;  Length 6;
  Best Local Similarity   100.0%;  Pred. No. 3e+05;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SVSEIQ 6
              ||||||
Db          1 SVSEIQ 6


RESULT 11
US-08-817-547A-4
; Sequence 4, Application US/08817547A
; Patent No. 6030790
;  GENERAL INFORMATION:
;    APPLICANT:  Adermann, Knut
;    APPLICANT:  Hock, Dieter
;    APPLICANT:  Magerlein, Markus
;    TITLE OF INVENTION:  Peptides from the hPTH Sequence
;    NUMBER OF SEQUENCES:  36
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Jones & Askew, LLP
;      STREET:  191 Peachtree Street, 37th Floor
;      CITY:  Atlanta
;      STATE:  Georgia
;      COUNTRY:  USA
;      ZIP:  30303
```

```
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/817,547A
;      FILING DATE:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/EP95/03757
;      FILING DATE:  29 SEPT 1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  FROST, ROGER T.
;      REGISTRATION NUMBER:  22,176
;      REFERENCE/DOCKET NUMBER:  07826-0007
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  404-818-3700
;      TELEFAX:  404-818-3799
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  7 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  unknown
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  peptide
;    HYPOTHETICAL:  no
;    ANTI-SENSE:  no
US-08-817-547A-4

  Query Match             42.6%;  Score 26;  DB 3;  Length 7;
  Best Local Similarity   100.0%;  Pred. No. 3e+05;
  Matches    6;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SVSEIQ 6
              ||||||
Db          1 SVSEIQ 6


RESULT 12
US-09-421-379-8
; Sequence 8, Application US/09421379
; Patent No. 6495662
; GENERAL INFORMATION:
;  APPLICANT: Gardella, Thomas J.
;  APPLICANT: Kronenberg, Henry
;  APPLICANT: Potts, John T.
;  APPLICANT: Juppner, Harald
;  TITLE OF INVENTION: Bioactive Peptides and Peptide Derivatives of
;  TITLE OF INVENTION: Parathyroid Hormone (PTH) and Parathyroid
;  TITLE OF INVENTION: Hormone-Related Peptide (PTHrP)
;  FILE REFERENCE: 0609.4570001
;  CURRENT APPLICATION NUMBER: US/09/421,379
;  CURRENT FILING DATE: 1999-10-20
;  EARLIER APPLICATION NUMBER: U.S. 60/105,530
;  EARLIER FILING DATE: 1998-10-22
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: synthetic
;   OTHER INFORMATION: peptide
US-09-421-379-8

  Query Match             42.6%;  Score 26;  DB 4;  Length 9;
  Best Local Similarity   55.6%;  Pred. No. 3e+05;
  Matches    5;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 SVSEIQFMH 9
              :||| | :|
Db          1 AVSEHQLLH 9


RESULT 13
US-08-482-228-42
; Sequence 42, Application US/08482228
; Patent No. 5968753
;  GENERAL INFORMATION:
;    APPLICANT:  Tseng-Law, Janet
;    APPLICANT:  Kobori, Joan A.
;    APPLICANT:  Al-Abdaly, Fahad A.
;    APPLICANT:  Guillermo, Roy
;    APPLICANT:  Helgerson, Sam L.
;    APPLICANT:  Deans, Robert J.
;    TITLE OF INVENTION:  POSITIVE AND POSITIVE/NEGATIVE CELL
;    TITLE OF INVENTION:  SELECTION MEDIATED BY PEPTIDE RELEASE
;    NUMBER OF SEQUENCES:  215
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Janice Guthrie, Ph.D.
;      STREET:  P.O. Box 15210
;      CITY:  Irvine
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  92713-5210
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/482,228
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Guthrie, Janice
;      REGISTRATION NUMBER:  35,170
;      REFERENCE/DOCKET NUMBER:  IT-4630CIP3
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (714) 440-5353
;      TELEFAX:  (714) 553-1952
;  INFORMATION FOR SEQ ID NO:  42:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  12 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-482-228-42

  Query Match             41.0%;  Score 25;  DB 2;  Length 12;
  Best Local Similarity   57.1%;  Pred. No. 1.3e+02;
  Matches    4;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          3 SEIQFMH 9
              | : |||
Db          5 SSVTFMH 11


RESULT 14
US-08-482-528-42
; Sequence 42, Application US/08482528
; Patent No. 6017719
;  GENERAL INFORMATION:
;    APPLICANT:  Tseng-Law, Janet
;    APPLICANT:  Kobori, Joan A.
;    APPLICANT:  Al-Abdaly, Fahad A.
;    APPLICANT:  Guillermo, Roy
;    APPLICANT:  Helgerson, Sam L.
;    APPLICANT:  Deans, Robert J.
;    TITLE OF INVENTION:  POSITIVE AND POSITIVE/NEGATIVE CELL
;    TITLE OF INVENTION:  SELECTION MEDIATED BY PEPTIDE RELEASE
;    NUMBER OF SEQUENCES:  215
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Janice Guthrie, Ph.D.
;      STREET:  P.O. Box 15210
```

```
;       CITY:  Irvine
;       STATE:  California
;       COUNTRY:  USA
;       ZIP:  92713-5210
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/482,528
;       FILING DATE:  07-JUN-1995
;       CLASSIFICATION:  435
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Guthrie, Janice
;       REGISTRATION NUMBER:  35,170
;       REFERENCE/DOCKET NUMBER:  IT-4630CIP4
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (714) 440-5353
;       TELEFAX:  (714) 553-1952
;   INFORMATION FOR SEQ ID NO:  42:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  12 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  peptide
US-08-482-528-42

  Query Match             41.0%;  Score 25;  DB 3;  Length 12;
  Best Local Similarity   57.1%;  Pred. No. 1.3e+02;
  Matches    4;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          3 SEIQFMH 9
              | : |||
Db          5 SSVTFMH 11


RESULT 15
US-08-177-109A-56
; Sequence 56, Application US/08177109A
; Patent No. 5869615
;  GENERAL INFORMATION:
;     APPLICANT:  Dennis E. Hourcade and Teresa J. Oglesby
;     TITLE OF INVENTION:  MODIFIED COMPLEMENT PROTEASES
;     NUMBER OF SEQUENCES:  62
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Patrea L. Pabst
;       STREET:  2800 One Atlantic Center
;       STREET:  1201 West Peachtree Street
;       CITY:  Atlanta
;       STATE:  Georgia
;       COUNTRY:  USA
;       ZIP:  30309-3450
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/177,109A
;       FILING DATE:  03-JAN-1994
;       CLASSIFICATION:  514
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Pabst, Patrea L.
;       REGISTRATION NUMBER:  31,284
;       REFERENCE/DOCKET NUMBER:  WU 107
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (404) 873-8794
;       TELEFAX:  (404) 873-8795
;   INFORMATION FOR SEQ ID NO:  56:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  5 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
;     HYPOTHETICAL:  NO
US-08-177-109A-56

  Query Match             39.3%;  Score 24;  DB 2;  Length 5;
  Best Local Similarity   60.0%;  Pred. No. 3e+05;
  Matches    3;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 MHNLG 12
              :||:|
Db          1 LHNMG 5


Search completed: September  5, 2004, 09:38:33
Job time : 12 secs
```

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: September 5, 2004, 09:30:43 ; Search time 9.5 Seconds
(without alignments)
121.505 Million cell updates/sec

Title: US-09-730-174A-5
Perfect score: 59
Sequence: 1 AVSEIQLMHNLG 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 1581

Minimum DB seq length: 0
Maximum DB seq length: 12

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	21	35.6	12	2	S21205	Ig heavy chain V r
2	18	30.5	7	2	A58718	carnocin UI49 - Ca
3	18	30.5	9	2	S78420	ribosomal protein
4	18	30.5	10	2	A60589	sperm-activating p
5	18	30.5	10	2	B46453	e antigen p20e pre
6	18	30.5	12	2	A55837	5-aminoimidazole r
7	17	28.8	7	2	I46868	alpha-myosin heavy
8	17	28.8	10	2	A37268	Ig heavy chain C r
9	17	28.8	12	2	PH1190	T-cell receptor al
10	17	28.8	12	2	PH1187	T-cell receptor al
11	17	28.8	12	2	PH1189	T-cell receptor al
12	16	27.1	10	2	A47364	placental lactogen
13	16	27.1	11	2	PH0924	T-cell receptor be
14	15	25.4	7	2	S25266	pilE protein - Esc
15	15	25.4	7	2	S29735	polyphosphate-gluc
16	15	25.4	9	2	PW0002	chlorophyll a/b-bi
17	15	25.4	9	2	A56029	N-methylpurine DNA
18	15	25.4	10	2	E49033	T-cell receptor ga
19	15	25.4	11	2	A38841	rhodopsin homolog
20	15	25.4	11	2	B41835	translation elonga
21	15	25.4	11	2	A40795	glycoprotein H-a -
22	14	23.7	4	2	I38888	COI intron 16 prot
23	14	23.7	7	2	T09512	NADH2 dehydrogenas
24	14	23.7	9	2	PT0238	Ig heavy chain CRD
25	14	23.7	10	1	SPPGNK	neuromedin K - pig
26	14	23.7	10	2	S28055	cytochrome b559 co
27	14	23.7	10	2	S27873	hypothetical prote
28	14	23.7	10	2	C61033	ranatachykinin C -
29	14	23.7	11	2	S71304	amine oxidase (cop
30	14	23.7	11	2	S60354	retinal oxidase -
31	14	23.7	11	2	B29806	acidic proline-ric
32	14	23.7	11	4	S41909	hypothetical prote
33	14	23.7	12	2	S25485	transcription fact
34	14	23.7	12	2	G49410	t-complex polypept
35	14	23.7	12	2	S71034	potB protein - Sal
36	14	23.7	12	2	PH1175	T-cell receptor al
37	14	23.7	12	2	PH1174	T-cell receptor al
38	14	23.7	12	2	I41235	glutamine-tRNA lig
39	13	22.0	6	2	PQ0008	angiotensin-conver
40	13	22.0	8	2	T14906	hypothetical prote
41	13	22.0	8	2	JS0316	leucokinin VI - Ma
42	13	22.0	8	2	PH1618	Ig H chain V-D-J r
43	13	22.0	9	2	S13636	coat protein beta
44	13	22.0	9	2	JN0026	sperm-activating p
45	13	22.0	9	2	PT0231	Ig heavy chain CDR

ALIGNMENTS

RESULT 1
S21205
Ig heavy chain V region - human
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 16-Aug-1996
C;Accession: S21205
R;Makiya, R.; Stigbrand, T.
Eur. J. Biochem. 205, 341-345, 1992
A;Title: Placental alkaline phosphatase has a binding site for the human immunoglobulin
A;Reference number: S21205; MUID:92209522; PMID:1555592
A;Accession: S21205
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-12 <MAK>
C;Keywords: heterotetramer; immunoglobulin

Query Match 35.6%; Score 21; DB 2; Length 12;
Best Local Similarity 44.4%; Pred. No. 6.9e+02;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

```
Qy          4 EIQLMHNLG 12
              |:||: : |
Db          1 EVQLVESGG 9
```

RESULT 2
A58718
carnocin UI49 - Carnobacterium sp. (fragment)
C;Species: Carnobacterium sp.
C;Date: 23-Jan-1998 #sequence_revision 30-Jan-1998 #text_change 30-Jan-1998
C;Accession: A58718
R;Stoffels, G.; Nissen-Meyer, J.; Gudmundsdottir, A.; Sletten, K.; Holo, H.; Nes, I.F.
Appl. Environ. Microbiol. 58, 1417-1422, 1992
A;Title: Purification and characterization of a new bacteriocin isolated from a Carnoba
A;Reference number: A58718; MUID:92321768; PMID:1622206
A;Accession: A58718
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-7 <STO>
C;Keywords: antibiotic; lanthionine

Query Match 30.5%; Score 18; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          3 SEIQ 6
              ||||
Db          2 SEIQ 5
```

RESULT 3
S78420

```
ribosomal protein RL41, mitochondrial [validated] - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 25-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 21-Jul-2000
C;Accession: S78420
R;Goldschmidt-Reisin, S.; Graack, H.R.
submitted to the Protein Sequence Database, February 1998
A;Reference number: S78411
A;Accession: S78420
A;Molecule type: protein
A;Residues: 1-9 <GOL>
A;Note: the protein is designated as mitochondrial ribosomal protein L41
C;Keywords: mitochondrion; protein biosynthesis; ribosome

  Query Match             30.5%;  Score 18;  DB 2;  Length 9;
  Best Local Similarity   75.0%;  Pred. No. 2.8e+05;
  Matches    3;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          9 HNLG 12
              | ||
Db          5 HRLG 8


RESULT 4
A60589
sperm-activating peptide (Tyr-2, Asn-3, Gly-5, Ile-9, Asp-10 SAP-I) - slate-pencil urchi
C;Species: Heterocentrotus mamillatus
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 18-Aug-2000
C;Accession: A60589
R;Yoshino, K.I.; Kajiura, H.; Nomura, K.; Takao, T.; Shimonishi, Y.; Kurita, M.; Yamaguc
Comp. Biochem. Physiol. B 94, 739-751, 1989
A;Title: A halogenated amino acid-containing sperm activating peptide and its related pe
otus nudus, Echinometra mathaei and Heterocentrotus mammillatus.
A;Reference number: A60527
A;Accession: A60589
A;Molecule type: protein
A;Residues: 1-10 <YOS>
C;Superfamily: unassigned animal peptides

  Query Match             30.5%;  Score 18;  DB 2;  Length 10;
  Best Local Similarity   75.0%;  Pred. No. 2.1e+03;
  Matches    3;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          9 HNLG 12
              :|||
Db          2 YNLG 5


RESULT 5
B46453
e antigen p20e precursor - hepatitis B virus (subtype adr) (fragment)
N;Alternate names: HBe antigen precursor
N;Contains: e antigen
C;Species: hepatitis B virus, HBV
A;Variety: subtype adr
C;Date: 18-Jun-1993 #sequence_revision 08-Nov-1996 #text_change 15-Aug-1997
C;Accession: B46453
R;Takahashi, K.; Kishimoto, S.; Ohori, K.; Yoshizawa, H.; Machida, A.; Ohnuma, H.; Tsuda
J. Immunol. 147, 3156-3160, 1991
A;Title: Molecular heterogeneity of e antigen polypeptides in sera from carriers of hepa
A;Reference number: A46453; MUID:92013147; PMID:1717588
A;Accession: B46453
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-10 <TAK>
A;Experimental source: subtype adr
A;Note: sequence extracted from NCBI backbone (NCBIP:60243)
F;1-10/Domain: signal sequence (fragment) #status predicted <SIG>

  Query Match             30.5%;  Score 18;  DB 2;  Length 10;
  Best Local Similarity   60.0%;  Pred. No. 2.1e+03;
  Matches    3;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          5 IQLMH 9
                :|| |
Db          1 MQLFH 5


RESULT 6
A55837
5-aminoimidazole ribonucleotide carboxylase/4-N-succinylamino carbonyl-5-aminoimidazole
C;Species: Gallus gallus (chicken)
C;Date: 19-Jan-1996 #sequence_revision 19-Jan-1996 #text_change 17-Mar-1999
C;Accession: A55837
R;Firestine, S.M.; Davisson, V.J.
Biochemistry 33, 11917-11926, 1994
A;Title: Carboxylases in de Novo purine biosynthesis. Characterization of the Gallus gal
A;Reference number: A55837; MUID:95001903; PMID:7918410
A;Accession: A55837
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-12 <FIR>

  Query Match             30.5%;  Score 18;  DB 2;  Length 12;
  Best Local Similarity   57.1%;  Pred. No. 2.6e+03;
  Matches    4;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 AVSEIQL 7
              | ||: |
Db          2 AASELAL 8


RESULT 7
I46868
alpha-myosin heavy chain - rabbit (fragment)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 14-Feb-1997 #sequence_revision 14-Feb-1997 #text_change 05-Nov-1999
C;Accession: I46868
R;Friedman, D.J.; Umeda, P.K.; Sinha, A.M.; Hsu, H.
Proc. Natl. Acad. Sci. U.S.A. 81, 3044-3048, 1984
A;Title: Characterization of genomic clones specifying rabbit alpha- and beta-ventricula
A;Reference number: I46868; MUID:84221901; PMID:6328491
A;Accession: I46868
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-7 <FRI>
A;Cross-references: GB:K01698; NID:g165538; PIDN:AAA31415.1; PID:g165539

  Query Match             28.8%;  Score 17;  DB 2;  Length 7;
  Best Local Similarity   60.0%;  Pred. No. 2.8e+05;
  Matches    3;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          6 QLMHN 10
              | ||:
Db          1 QKMHD 5


RESULT 8
A37268
Ig heavy chain C region (129) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 19-Mar-1997 #sequence_revision 13-Mar-1998 #text_change 13-Mar-1998
C;Accession: A37268
R;Ruff-Jamison, S.; Campos-Gonzalez, R.; Glenney Jr., J.R.
J. Biol. Chem. 266, 6607-6613, 1991
A;Title: Heavy and light chain variable region sequences and antibody properties of anti
A;Reference number: A38740; MUID:91177923; PMID:1706720
A;Accession: A37268
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-10 <RUF>

  Query Match             28.8%;  Score 17;  DB 2;  Length 10;
  Best Local Similarity   44.4%;  Pred. No. 3.3e+03;
  Matches    4;  Conservative    1;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          4 EIQLMHNLG 12
```

```
                  | |   |:|
Db          1 ESQSFPNVG 9
```

RESULT 9
PH1190
T-cell receptor alpha chain V region (Cw3/10.1) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
C;Accession: PH1190
R;Casanova, J.L.; Cerottini, J.C.; Matthes, M.; Necker, A.; Gournier, H.; Barra, C.; Wid
J. Exp. Med. 176, 439-447, 1992
A;Title: H-2-restricted cytolytic T lymphocytes specific for HLA display T cell receptor
A;Reference number: S26512; MUID:92364546; PMID:1380061
A;Accession: PH1190
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-12 <CAS>

Query Match 28.8%; Score 17; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 AVSE 4
              ||||
Db          2 AVSE 5
```

RESULT 10
PH1187
T-cell receptor alpha chain V region (Cw3/1F11) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
C;Accession: PH1187
R;Casanova, J.L.; Cerottini, J.C.; Matthes, M.; Necker, A.; Gournier, H.; Barra, C.; Wid
J. Exp. Med. 176, 439-447, 1992
A;Title: H-2-restricted cytolytic T lymphocytes specific for HLA display T cell receptor
A;Reference number: S26512; MUID:92364546; PMID:1380061
A;Accession: PH1187
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-12 <CAS>

Query Match 28.8%; Score 17; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 AVSE 4
              ||||
Db          2 AVSE 5
```

RESULT 11
PH1189
T-cell receptor alpha chain V region (Cw3/2C3) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
C;Accession: PH1189
R;Casanova, J.L.; Cerottini, J.C.; Matthes, M.; Necker, A.; Gournier, H.; Barra, C.; Wid
J. Exp. Med. 176, 439-447, 1992
A;Title: H-2-restricted cytolytic T lymphocytes specific for HLA display T cell receptor
A;Reference number: S26512; MUID:92364546; PMID:1380061
A;Accession: PH1189
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-12 <CAS>

Query Match 28.8%; Score 17; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 AVSE 4
              ||||
Db          2 AVSE 5
```

RESULT 12
A47364
placental lactogen-I precursor - mouse (fragment)
C;Species: Mus sp. (mouse)
C;Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 12-Aug-1996
C;Accession: A47364
R;Shida, M.M.; Ng, Y.K.; Soares, M.J.; Linzer, D.I.
Mol. Endocrinol. 7, 181-188, 1993
A;Title: Trophoblast-specific transcription from the mouse placental lactogen-I gene pr
A;Reference number: A47364; MUID:93225959; PMID:8469232
A;Accession: A47364
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-10 <RES>
A;Cross-references: GB:S58124; NID:g299449

Query Match 27.1%; Score 16; DB 2; Length 10;
Best Local Similarity 57.1%; Pred. No. 5.1e+03;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

```
Qy          5 IQLMHNL 11
              :||  ||
Db          1 MQLTLNL 7
```

RESULT 13
PH0924
T-cell receptor beta chain V-D-J region (isolate 10) - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997
C;Accession: PH0924
R;Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.
J. Exp. Med. 174, 1467-1476, 1991
A;Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allerg
A;Reference number: PH0891; MUID:92078857; PMID:1836012
A;Accession: PH0924
A;Molecule type: mRNA
A;Residues: 1-11 <GOL>
A;Experimental source: concanavalin A-activated lymphoblast
C;Keywords: T-cell receptor

Query Match 27.1%; Score 16; DB 2; Length 11;
Best Local Similarity 50.0%; Pred. No. 5.7e+03;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

```
Qy          1 AVSEIQLM 8
              | | : ||
Db          2 ASSSMDLM 9
```

RESULT 14
S25266
pilE protein - Escherichia coli (fragment)
C;Species: Escherichia coli
C;Date: 28-May-1993 #sequence_revision 28-May-1993 #text_change 11-Jun-1993
C;Accession: S25266
R;Dupuy, B.; Taha, M.K.; Possot, O.; Marchal, C.; Pugsley, A.P.
Mol. Microbiol. 6, 1887-1894, 1992
A;Title: PulO, a component of the pullulanase secretion pathway of Klebsiella oxytoca,
A;Reference number: S25266; MUID:92374839; PMID:1354833
A;Accession: S25266
A;Molecule type: protein
A;Residues: 1-7 <DUP>
C;Genetics:
A;Gene: pilE

Query Match 25.4%; Score 15; DB 2; Length 7;
Best Local Similarity 75.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```
Qy          5 IQLM 8
              |:||
Db          4 IELM 7
```

RESULT 15
S29735
polyphosphate-glucose phosphotransferase (EC 2.7.1.63) - Propionibacterium freudenreichi
C;Species: Propionibacterium freudenreichii subsp. shermanii
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 03-Jun-2002
C;Accession: S29735
R;Phillips, N.F.B.; Horn, P.J.; Wood, H.G.
Arch. Biochem. Biophys. 300, 309-319, 1993
A;Title: The polyphosphate- and ATP-dependent glucokinase from Propionibacterium sherman
A;Reference number: S29735; MUID:93143332; PMID:8380966
A;Accession: S29735
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-7 <PHI>
C;Keywords: phosphotransferase

  Query Match 25.4%; Score 15; DB 2; Length 7;
  Best Local Similarity 75.0%; Pred. No. 2.8e+05;
  Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy          9 HNLG 12
              | ||
Db          2 HVLG 5
```

Search completed: September 5, 2004, 09:37:44
Job time : 9.5 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: September 5, 2004, 09:27:07 ; Search time 6.5 Seconds
(without alignments)
96.130 Million cell updates/sec

Title: US-09-730-174A-5
Perfect score: 59
Sequence: 1 AVSEIQLMHNLG 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 501

Minimum DB seq length: 0
Maximum DB seq length: 12

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	18	30.5	7	1	LANC_CARUI	P36960 carnobacter
2	16	27.1	8	1	ALL6_CYDPO	P82157 cydia pomon
3	16	27.1	8	1	FUSS_FUSSO	P81010 fusarium so
4	16	27.1	11	1	EFG_CLOPA	P81350 clostridium
5	15	25.4	11	1	PVK1_PERAM	P41837 periplaneta
6	14	23.7	6	1	TRPI_PSEPU	P36414 pseudomonas
7	14	23.7	7	1	ALL7_CYDPO	P82158 cydia pomon
8	14	23.7	8	1	AL18_CARMA	P81821 carcinus ma
9	14	23.7	8	1	ALL1_CYDPO	P82152 cydia pomon
10	14	23.7	9	1	FAR8_MACRS	P83281 macrobrachi
11	14	23.7	9	1	UF02_MOUSE	P38640 mus musculu
12	14	23.7	10	1	AL19_CARMA	P81822 carcinus ma
13	14	23.7	10	1	PSBF_CAPAN	Q03367 capsicum an
14	14	23.7	10	1	TEMK_RANTE	P56923 rana tempor
15	14	23.7	10	1	TKNC_RANCA	P22690 rana catesb
16	14	23.7	10	1	TKNK_PIG	P01292 sus scrofa
17	14	23.7	11	1	ASL1_BACSE	P83146 bacteroides
18	14	23.7	12	1	CD11_LITXA	P56245 litoria xan
19	14	23.7	12	1	CD14_LITXA	P56246 litoria xan
20	14	23.7	12	1	PORD_METTM	P80903 methanobact
21	14	23.7	12	1	RS19_TOBBP	Q56251 tomato big
22	13	22.0	8	1	LCK4_LEUMA	P21143 leucophaea
23	13	22.0	8	1	LCK6_LEUMA	P19988 leucophaea
24	13	22.0	9	1	MOSH_CLYJA	P19852 clypeaster
25	13	22.0	9	1	PPK1_PERAM	P82691 periplaneta
26	13	22.0	10	1	RRPL_PHODV	P35946 phocine dis
27	13	22.0	11	1	CSI5_BACSU	P81095 bacillus su
28	13	22.0	11	1	Q2OA_COMTE	P80464 comamonas t
29	13	22.0	12	1	PPK4_PERFU	P82690 periplaneta
30	12	20.3	9	1	FIBB_PAPHA	P19343 papio hamad
31	12	20.3	9	1	RE42_LITRU	P82075 litoria rub
32	12	20.3	10	1	GLEM_HUMAN	P02728 homo sapien
33	12	20.3	10	1	GON1_CLUPA	P81749 clupea pall
34	12	20.3	10	1	GON2_CHEPR	P80678 chelyosoma
35	12	20.3	10	1	HTF1_ROMMI	P18110 romalea mic
36	12	20.3	10	1	HTF_HELZE	P16353 heliothis z
37	12	20.3	10	1	SYK_CAMUP	Q46464 campylobact
38	12	20.3	10	1	TKNB_RANRI	P29135 rana ridibu
39	12	20.3	11	1	CXL1_CONMR	P58807 conus marmo
40	12	20.3	11	1	HS70_PINPS	P81672 pinus pinas
41	12	20.3	11	1	T2P1_PROVU	P31031 proteus vul
42	12	20.3	12	1	HEP1_BACSE	P83054 bacteroides
43	12	20.3	12	1	PPK4_PERAM	P82619 periplaneta
44	11	18.6	7	1	TY51_LITRU	P82065 litoria rub
45	11	18.6	7	1	UN06_PINPS	P81675 pinus pinas

ALIGNMENTS

RESULT 1
LANC_CARUI
ID LANC_CARUI STANDARD; PRT; 7 AA.
AC P36960;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Lantibiotic carnocin UI49 (Fragment).
OS Carnobacterium sp. (strain UI49).
OC Bacteria; Firmicutes; Lactobacillales; Carnobacteriaceae;
OC Carnobacterium.
OX NCBI_TaxID=35782;
RN [1]
RP SEQUENCE.
RX MEDLINE=92321768; PubMed=1622206;
RA Stoffels G., Nissen-Meyer J., Gudmundsdottir A., Sletten K., Holo H.,
RA Nes I.F.;
RT "Purification and characterization of a new bacteriocin isolated from
RT a Carnobacterium sp.";
RL Appl. Environ. Microbiol. 58:1417-1422(1992).
CC -!- FUNCTION: Lanthionine-containing peptide antibiotic (lantibiotic).
CC Active on Gram-positive bacteria.
KW Antibiotic; Bacteriocin; Lantibiotic.
FT NON_TER 7 7
SQ SEQUENCE 7 AA; 786 MW; 741776D05B05B810 CRC64;

Query Match 30.5%; Score 18; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.4e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SEIQ 6
||||
Db 2 SEIQ 5

RESULT 2
ALL6_CYDPO
ID ALL6_CYDPO STANDARD; PRT; 8 AA.
AC P82157;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Cydiastatin 6.
OS Cydia pomonella (Codling moth).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC Tortricoidea; Tortricidae; Olethreutinae; Cydia.
OX NCBI_TaxID=82600;
RN [1]
RP SEQUENCE.
RC TISSUE=Larva;
RX MEDLINE=98054539; PubMed=9392829;
RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Winstanley D.,
RA Davey M., East P.D., Thorpe A.;
RT "Lepidopteran peptides of the allatostatin superfamily.";
RL Peptides 18:1301-1309(1997).

```
CC   -!- SIMILARITY: Belongs to the allatostatin family.
KW   Neuropeptide; Amidation.
FT   MOD_RES       8       8       AMIDATION.
SQ   SEQUENCE   8 AA;  936 MW;  0B2879C45B573767 CRC64;

  Query Match             27.1%;  Score 16;  DB 1;  Length 8;
  Best Local Similarity   40.0%;  Pred. No. 1.4e+05;
  Matches    2;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          8 MHNLG 12
              ::| |
Db          3 LYNFG 7


RESULT 3
FUSS_FUSSO
ID   FUSS_FUSSO     STANDARD;      PRT;     8 AA.
AC   P81010;
DT   15-JUL-1998 (Rel. 36, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Allergen Fus s I3596* (Fragment).
OS   Fusarium solani (subsp. pisi) (Nectria haematococca).
OC   Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC   Hypocreomycetidae; Hypocreales; Nectriaceae; Nectria.
OX   NCBI_TaxID=70791;
RN   [1]
RP   SEQUENCE.
RC   STRAIN=IARI 3596; TISSUE=Mycelium;
RA   Verma J., Gangal S.V.;
RL   Submitted (JUL-1997) to Swiss-Prot.
CC   -!- ALLERGEN: Causes an allergic reaction in human.
KW   Allergen.
FT   NON_TER       8       8
SQ   SEQUENCE   8 AA;  898 MW;  C372C441F5B69041 CRC64;

  Query Match             27.1%;  Score 16;  DB 1;  Length 8;
  Best Local Similarity   40.0%;  Pred. No. 1.4e+05;
  Matches    2;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 LMHNL 11
              : ||:
Db          3 MSHNV 7


RESULT 4
EFG_CLOPA
ID   EFG_CLOPA      STANDARD;      PRT;    11 AA.
AC   P81350;
DT   15-JUL-1998 (Rel. 36, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Elongation factor G (EF-G) (CP 5) (Fragment).
GN   FUSA.
OS   Clostridium pasteurianum.
OC   Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC   Clostridium.
OX   NCBI_TaxID=1501;
RN   [1]
RP   SEQUENCE.
RC   STRAIN=W5;
RX   MEDLINE=98291870; PubMed=9629918;
RA   Flengsrud R., Skjeldal L.;
RT   "Two-dimensional gel electrophoresis separation and N-terminal
RT   sequence analysis of proteins from Clostridium pasteurianum W5.";
RL   Electrophoresis 19:802-806(1998).
CC   -!- FUNCTION: This protein promotes the GTP-dependent translocation of
CC       the nascent protein chain from the A-site to the P-site of the
CC       ribosome.
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC   -!- SIMILARITY: Belongs to the GTP-binding elongation factor family.
CC       EF-G/EF-2 subfamily.
DR   InterPro; IPR000795; EF_GTPbind.
DR   PROSITE; PS00301; EFACTOR_GTP; PARTIAL.
KW   Elongation factor; Protein biosynthesis; GTP-binding.
FT   NON_TER      11      11
SQ   SEQUENCE   11 AA;  1337 MW;  412E71F1D9C33B17 CRC64;

  Query Match             27.1%;  Score 16;  DB 1;  Length 11;
  Best Local Similarity   25.0%;  Pred. No. 3.5e+03;
  Matches    2;  Conservative    3;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          5 IQLMHNLG 12
              ::   |:|
Db          4 LEKFQNIG 11


RESULT 5
PVK1_PERAM
ID   PVK1_PERAM     STANDARD;      PRT;    11 AA.
AC   P41837;
DT   01-NOV-1995 (Rel. 32, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Periviscerokinin-1 (Pea-PVK-1).
OS   Periplaneta americana (American cockroach).
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattoidea;
OC   Blattidae; Periplaneta.
OX   NCBI_TaxID=6978;
RN   [1]
RP   SEQUENCE, AND SYNTHESIS.
RC   TISSUE=Abdominal perisympathetic organs;
RX   MEDLINE=95232021; PubMed=7716075;
RA   Predel R., Linde D., Rapus J., Vettermann S., Penzlin H.;
RT   "Periviscerokinin (Pea-PVK): a novel myotropic neuropeptide from the
RT   perisympathetic organs of the American cockroach.";
RL   Peptides 16:61-66(1995).
CC   -!- FUNCTION: MYOACTIVE PEPTIDE; HAS EXCITORY ACTIONS ON THE
CC       HYPERNEURAL MUSCLE.
KW   Neuropeptide; Amidation.
FT   MOD_RES      11      11      AMIDATION.
SQ   SEQUENCE   11 AA;  1114 MW;  39DB5419D7605728 CRC64;

  Query Match             25.4%;  Score 15;  DB 1;  Length 11;
  Best Local Similarity   50.0%;  Pred. No. 5.5e+03;
  Matches    3;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          5 IQLMHN 10
              | :| |
Db          6 IPVMRN 11


RESULT 6
TRPI_PSEPU
ID   TRPI_PSEPU     STANDARD;      PRT;     6 AA.
AC   P36414;
DT   01-JUN-1994 (Rel. 29, Created)
DT   01-JUN-1994 (Rel. 29, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   HTH-type transcriptional regulator trpI (TrpBA operon transcriptional
DE   activator) (Fragment).
GN   TRPI.
OS   Pseudomonas putida.
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC   Pseudomonadaceae; Pseudomonas.
OX   NCBI_TaxID=303;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=PPG1 C1S;
RX   MEDLINE=89335826; PubMed=2503057;
RA   Eberly L., Crawford I.P.;
RT   "DNA sequence of the tryptophan synthase genes of Pseudomonas
RT   putida.";
RL   Biochimie 71:521-531(1989).
CC   -!- FUNCTION: ACTIVATES THE EXPRESSION OF THE TRPBA GENES ENCODING
```

```
CC       THE TWO TRYPTOPHAN SYNTHASE SUBUNITS. IN THE ABSENCE OF THE
CC       INDUCER (INDOLEGLYCEROL PHOSPHATE), TRPI BINDS UPSTREAM OF THE
CC       TRPAB OPERON, OVERLAPPING ITS OWN PROMOTER REGION.
CC   -!- SIMILARITY: Contains 1 HTH lysR-type DNA-binding domain.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X13299; CAA31660.1; -.
DR   InterPro; IPR000847; HTH_LysR.
DR   PROSITE; PS50931; HTH_LYSR; PARTIAL.
KW   Tryptophan biosynthesis; Transcription regulation; Activator;
KW   DNA-binding.
FT   NON_TER       6      6
SQ   SEQUENCE   6 AA;  683 MW;  77672AA1EDD6F000 CRC64;

  Query Match             23.7%;  Score 14;  DB 1;  Length 6;
  Best Local Similarity   40.0%;  Pred. No. 1.4e+05;
  Matches    2;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 LMHNL 11
              : |:|
Db          1 MAHDL 5


RESULT 7
ALL7_CYDPO
ID   ALL7_CYDPO     STANDARD;      PRT;     7 AA.
AC   P82158;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   Cydiastatin 7.
OS   Cydia pomonella (Codling moth).
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC   Tortricoidea; Tortricidae; Olethreutinae; Cydia.
OX   NCBI_TaxID=82600;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Larva;
RX   MEDLINE=98054539; PubMed=9392829;
RA   Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Winstanley D.,
RA   Davey M., East P.D., Thorpe A.;
RT   "Lepidopteran peptides of the allatostatin superfamily.";
RL   Peptides 18:1301-1309(1997).
CC   -!- SIMILARITY: Belongs to the allatostatin family.
KW   Neuropeptide; Amidation.
FT   MOD_RES       7      7       AMIDATION.
SQ   SEQUENCE   7 AA;  873 MW;  672879CABB569350 CRC64;

  Query Match             23.7%;  Score 14;  DB 1;  Length 7;
  Best Local Similarity   40.0%;  Pred. No. 1.4e+05;
  Matches    2;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          8 MHNLG 12
              |:: |
Db          2 MYDFG 6


RESULT 8
AL18_CARMA
ID   AL18_CARMA     STANDARD;      PRT;     8 AA.
AC   P81821;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   Carcinustatin 18.
OS   Carcinus maenas (Common shore crab) (Green crab).
OC   Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC   Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC   Eubrachyura; Portunoidea; Portunidae; Carcinus.
OX   NCBI_TaxID=6759;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Cerebral ganglion, and Thoracic ganglion;
RX   MEDLINE=98121193; PubMed=9461295;
RA   Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
RA   Thorpe A.;
RT   "Isolation and identification of multiple neuropeptides of the
RT   allatostatin superfamily in the shore crab Carcinus maenas.";
RL   Eur. J. Biochem. 250:727-734(1997).
CC   -!- FUNCTION: May act as a neurotransmitter or neuromodulator.
CC   -!- SIMILARITY: Belongs to the allatostatin family.
KW   Neuropeptide; Amidation; Multigene family.
FT   MOD_RES       8      8       AMIDATION (POTENTIAL).
SQ   SEQUENCE   8 AA;  919 MW;  C82879D5AB569AB5 CRC64;

  Query Match             23.7%;  Score 14;  DB 1;  Length 8;
  Best Local Similarity   40.0%;  Pred. No. 1.4e+05;
  Matches    2;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          8 MHNLG 12
              |:: |
Db          3 MYSFG 7


RESULT 9
ALL1_CYDPO
ID   ALL1_CYDPO     STANDARD;      PRT;     8 AA.
AC   P82152;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   Cydiastatin 1.
OS   Cydia pomonella (Codling moth).
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC   Tortricoidea; Tortricidae; Olethreutinae; Cydia.
OX   NCBI_TaxID=82600;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Larva;
RX   MEDLINE=98054539; PubMed=9392829;
RA   Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Winstanley D.,
RA   Davey M., East P.D., Thorpe A.;
RT   "Lepidopteran peptides of the allatostatin superfamily.";
RL   Peptides 18:1301-1309(1997).
CC   -!- SIMILARITY: Belongs to the allatostatin family.
KW   Neuropeptide; Amidation.
FT   MOD_RES       8      8       AMIDATION.
SQ   SEQUENCE   8 AA;  934 MW;  C82879C45B51F775 CRC64;

  Query Match             23.7%;  Score 14;  DB 1;  Length 8;
  Best Local Similarity   50.0%;  Pred. No. 1.4e+05;
  Matches    2;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          9 HNLG 12
              :| |
Db          4 YNFG 7


RESULT 10
FAR8_MACRS
ID   FAR8_MACRS     STANDARD;      PRT;     9 AA.
AC   P83281;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   FMRFamide-like neuropeptide FLP8 (VSHNNFLRF-amide).
OS   Macrobrachium rosenbergii (Giant fresh water prawn).
```

```
OC   Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC   Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Caridea;
OC   Palaemonoidea; Palaemonidae; Macrobrachium.
OX   NCBI_TaxID=79674;
RN   [1]
RP   SEQUENCE, AND MASS SPECTROMETRY.
RC   TISSUE=Eyestalk;
RX   MEDLINE=21107394; PubMed=11179812;
RA   Sithigorngul P., Saraithongkum W., Longyant S., Panchan N.,
RA   Sithigorngul W., Petsom A.;
RT   "Three more novel FMRFamide-like neuropeptide sequences from the
RT   eyestalk of the giant freshwater prawn Macrobrachium rosenbergii.";
RL   Peptides 22:191-197(2001).
CC   -!- MASS SPECTROMETRY: MW=1133.8; METHOD=MALDI.
CC   -!- SIMILARITY: Belongs to the FARP (FMRFamide related peptide)
CC       family.
DR   GO; GO:0007218; P:neuropeptide signaling pathway; IDA.
KW   Neuropeptide; Amidation.
FT   MOD_RES       9       9       AMIDATION.
SQ   SEQUENCE   9 AA;  1133 MW;  845A0729C44441F5 CRC64;

  Query Match             23.7%;  Score 14;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+05;
  Matches    2;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          9 HN 10
              ||
Db          3 HN 4


RESULT 11
UF02_MOUSE
ID   UF02_MOUSE     STANDARD;      PRT;     9 AA.
AC   P38640;
DT   01-OCT-1994 (Rel. 30, Created)
DT   01-OCT-1994 (Rel. 30, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Unknown protein from 2D-page of fibroblasts (P32) (Fragment).
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Fibroblast;
RX   MEDLINE=95009907; PubMed=7523108;
RA   Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;
RT   "Separation and sequencing of familiar and novel murine proteins
RT   using preparative two-dimensional gel electrophoresis.";
RL   Electrophoresis 15:735-745(1994).
CC   -!- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
CC       protein is: 6.0, its MW is: 32 kDa.
FT   NON_TER       9       9
SQ   SEQUENCE   9 AA;  1102 MW;  7E73EAB6D05B1AAB CRC64;

  Query Match             23.7%;  Score 14;  DB 1;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+05;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 EIQ 6
              |||
Db          4 EIQ 6


RESULT 12
AL19_CARMA
ID   AL19_CARMA     STANDARD;      PRT;     10 AA.
AC   P81822;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   Carcinustatin 19.
OS   Carcinus maenas (Common shore crab) (Green crab).
OC   Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC   Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC   Eubrachyura; Portunoidea; Portunidae; Carcinus.
OX   NCBI_TaxID=6759;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Cerebral ganglion, and Thoracic ganglion;
RX   MEDLINE=98121193; PubMed=9461295;
RA   Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
RA   Thorpe A.;
RT   "Isolation and identification of multiple neuropeptides of the
RT   allatostatin superfamily in the shore crab Carcinus maenas.";
RL   Eur. J. Biochem. 250:727-734(1997).
CC   -!- FUNCTION: May act as a neurotransmitter or neuromodulator.
CC   -!- SIMILARITY: Belongs to the allatostatin family.
KW   Neuropeptide; Amidation; Multigene family.
FT   MOD_RES      10      10       AMIDATION (POTENTIAL).
SQ   SEQUENCE   10 AA;  1101 MW;  96687CD5AB569AB1 CRC64;

  Query Match             23.7%;  Score 14;  DB 1;  Length 10;
  Best Local Similarity   40.0%;  Pred. No. 7.7e+03;
  Matches    2;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          8 MHNLG 12
              |:: |
Db          5 MYSFG 9


RESULT 13
PSBF_CAPAN
ID   PSBF_CAPAN     STANDARD;      PRT;     10 AA.
AC   Q03367;
DT   01-JUN-1994 (Rel. 29, Created)
DT   01-JUN-1994 (Rel. 29, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Cytochrome b559 beta subunit (PSII reaction center subunit VI)
DE   (Fragment).
GN   PSBF.
OS   Capsicum annuum (Bell pepper).
OG   Chloroplast.
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC   lamiids; Solanales; Solanaceae; Capsicum.
OX   NCBI_TaxID=4072;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=cv. Lamuyo; TISSUE=Fruit, and Leaf;
RX   MEDLINE=93099270; PubMed=1463853;
RA   Kuntz M., Camara B., Weil J.-H., Schantz R.;
RT   "The psbL gene from bell pepper (Capsicum annuum): plastid RNA
RT   editing also occurs in non-photosynthetic chromoplasts.";
RL   Plant Mol. Biol. 20:1185-1188(1992).
CC   -!- FUNCTION: This b-type cytochrome is tightly associated with the
CC       reaction center of photosystem II and possibly is part of the
CC       water-oxidation complex.
CC   -!- SUBUNIT: Heterodimer of an alpha subunit and a beta subunit.
CC   -!- SIMILARITY: Belongs to the psbE / psbF family.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; X65570; CAA46539.1; -.
DR   PIR; S28055; S28055.
DR   HAMAP; MF_00643; -; 1.
DR   InterPro; IPR006216; Cyt_b559.
DR   PROSITE; PS00537; CYTOCHROME_B559; PARTIAL.
KW   Chloroplast; Photosystem II; Heme; Electron transport; Transmembrane.
FT   NON_TER       1       1
```

```
FT   TRANSMEM      <1       5       BY SIMILARITY.
FT   DOMAIN         6      10       LUMENAL (POTENTIAL).
SQ   SEQUENCE   10 AA;  1180 MW;  817D0F59D6D69DC5 CRC64;

  Query Match             23.7%;  Score 14;  DB 1;  Length 10;
  Best Local Similarity   25.0%;  Pred. No. 7.7e+03;
  Matches    2;  Conservative    4;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 AVSEIQLM 8
              ::| :| :
Db          1 SISAMQFI 8


RESULT 14
TEMK_RANTE
ID   TEMK_RANTE     STANDARD;      PRT;    10 AA.
AC   P56923;
DT   30-MAY-2000 (Rel. 39, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Temporin K.
OS   Rana temporaria (European common frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX   NCBI_TaxID=8407;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Skin secretion;
RX   MEDLINE=97175050; PubMed=9022710;
RA   Simmaco M., Mignogna G., Canofeni S., Miele R., Mangoni M.L.,
RA   Barra D.;
RT   "Temporins, antimicrobial peptides from the European red frog Rana
RT   temporaria.";
RL   Eur. J. Biochem. 242:788-792(1996).
CC   -!- FUNCTION: Has antibacterial activity against Gram-positive
CC       bacteria.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- TISSUE SPECIFICITY: Skin.
CC   -!- SIMILARITY: Belongs to the brevinin family.
KW   Amphibian defense peptide; Antibiotic; Amidation.
FT   MOD_RES       10      10       AMIDATION.
SQ   SEQUENCE   10 AA;  1123 MW;  390549B337272457 CRC64;

  Query Match             23.7%;  Score 14;  DB 1;  Length 10;
  Best Local Similarity   60.0%;  Pred. No. 7.7e+03;
  Matches    3;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 LMHNL 11
              |: ||
Db          1 LLPNL 5


RESULT 15
TKNC_RANCA
ID   TKNC_RANCA     STANDARD;      PRT;    10 AA.
AC   P22690;
DT   01-AUG-1991 (Rel. 19, Created)
DT   01-AUG-1991 (Rel. 19, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Ranatachykinin C (RTK C).
OS   Rana catesbeiana (Bull frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX   NCBI_TaxID=8400;
RN   [1]
RP   SEQUENCE, AND SYNTHESIS.
RC   TISSUE=Intestine;
RX   MEDLINE=91254337; PubMed=2043143;
RA   Kozawa H., Hino J., Minamino N., Kangawa K., Matsuo H.;
RT   "Isolation of four novel tachykinins from frog (Rana catesbeiana)
RT   brain and intestine.";
RL   Biochem. Biophys. Res. Commun. 177:588-595(1991).
RN   [2]
RP   SEQUENCE.
RC   TISSUE=Intestine;
RX   MEDLINE=94023216; PubMed=8210506;
RA   Kangawa K., Kozawa H., Hino J., Minamino N., Matsuo H.;
RT   "Four novel tachykinins in frog (Rana catesbeiana) brain and
RT   intestine.";
RL   Regul. Pept. 46:81-88(1993).
CC   -!- FUNCTION: Tachykinins are active peptides which excite neurons,
CC       evoke behavioral responses, are potent vasodilators and
CC       secretagogues, and contract (directly or indirectly) many smooth
CC       muscles.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: Belongs to the tachykinin family.
DR   PIR; C61033; C61033.
DR   InterPro; IPR002040; Tachy_Neurokinin.
DR   PROSITE; PS00267; TACHYKININ; 1.
KW   Tachykinin; Neuropeptide; Amidation.
FT   MOD_RES       10      10       AMIDATION.
SQ   SEQUENCE   10 AA;  1086 MW;  3A3A407059D5BDC7 CRC64;

  Query Match             23.7%;  Score 14;  DB 1;  Length 10;
  Best Local Similarity   100.0%;  Pred. No. 7.7e+03;
  Matches    2;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          9 HN 10
              ||
Db          1 HN 2


Search completed: September  5, 2004, 09:35:03
Job time : 6.5 secs
```

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: September 5, 2004, 09:30:03 ; Search time 27.5 Seconds
(without alignments)
137.681 Million cell updates/sec

Title: US-09-730-174A-5
Perfect score: 59
Sequence: 1 AVSEIQLMHNLG 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 2565

Minimum DB seq length: 0
Maximum DB seq length: 12

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_25:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	27	45.8	11	13	Q9PS71	Q9ps71 agkistrodon
2	23	39.0	12	13	P82081	P82081 limnodynast
3	20	33.9	8	13	P82082	P82082 limnodynast
4	20	33.9	8	13	P82083	P82083 limnodynast
5	20	33.9	12	13	P82085	P82085 limnodynast
6	19	32.2	8	8	Q34909	Q34909 locusta mig
7	19	32.2	9	12	O92766	O92766 canine dist
8	19	32.2	9	12	O71066	O71066 canine dist
9	18	30.5	8	10	Q40659	Q40659 oryza sativ
10	18	30.5	10	12	Q9PXC3	Q9pxc3 hepatitis b
11	18	30.5	11	5	Q23876	Q23876 dictyosteli
12	18	30.5	12	15	Q85631	Q85631 avian carci
13	17	28.8	7	6	Q28742	Q28742 oryctolagus
14	17	28.8	9	4	Q15891	Q15891 homo sapien
15	17	28.8	9	8	Q9GD12	Q9gd12 linospadix
16	17	28.8	9	8	Q9GCV6	Q9gcv6 sclerosperm
17	17	28.8	11	10	P82336	P82336 pisum sativ
18	17	28.8	11	13	Q9PST1	Q9pst1 fugu rubrip
19	16	27.1	8	3	Q05403	Q05403 saccharomyc
20	16	27.1	8	4	Q15894	Q15894 homo sapien
21	16	27.1	9	2	Q44377	Q44377 aeromonas t
22	16	27.1	9	2	Q44468	Q44468 aeromonas v
23	16	27.1	9	2	Q8RKU3	Q8rku3 borrelia bu
24	16	27.1	9	2	Q43928	Q43928 aeromonas p
25	16	27.1	9	2	Q44001	Q44001 aeromonas e
26	16	27.1	9	2	Q9K4M6	Q9k4m6 staphylococ
27	16	27.1	9	10	Q9FXL0	Q9fxl0 lilium long
28	16	27.1	10	2	Q7WUG1	Q7wug1 pseudomonas
29	16	27.1	10	10	P82132	P82132 spinacia ol
30	16	27.1	10	10	P82133	P82133 spinacia ol
31	16	27.1	10	13	P82080	P82080 limnodynast
32	16	27.1	12	2	Q9X6Y0	Q9x6y0 aquifex pyr
33	15	25.4	7	12	Q66205	Q66205 transmissib
34	15	25.4	8	13	P82079	P82079 limnodynast
35	15	25.4	9	2	Q43960	Q43960 azotobacter
36	15	25.4	9	5	Q8WTI9	Q8wti9 drosophila
37	15	25.4	10	6	Q9TS43	Q9ts43 sus scrofa
38	15	25.4	10	8	Q8WBR7	Q8wbr7 chaitophoru
39	15	25.4	11	6	Q9BDC8	Q9bdc8 pongo pygma
40	15	25.4	11	6	Q9BDQ9	Q9bdq9 gorilla gor
41	15	25.4	11	6	Q9BDD0	Q9bdd0 pan troglod
42	15	25.4	11	6	Q9BDC9	Q9bdc9 pan paniscu
43	15	25.4	12	6	Q9TQY5	Q9tqy5 bos taurus
44	15	25.4	12	11	Q9EQV3	Q9eqv3 mus musculu
45	14	23.7	8	2	Q49534	Q49534 mycoplasma

ALIGNMENTS

RESULT 1
Q9PS71
ID Q9PS71 PRELIMINARY; PRT; 11 AA.
AC Q9PS71;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Fibrinolytic metalloproteinase (Fragment).
OS Agkistrodon contortrix.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Agkistrodon.
OX NCBI_TaxID=8720;
RN [1]
RP SEQUENCE.
RX MEDLINE=91378546; PubMed=1898066;
RA Guan A.L., Retzios A.D., Henderson G.N., Markland F.S.Jr.;
RT "Purification and characterization of a fibrinolytic enzyme from venom
RT of the southern copperhead snake (Agkistrodon contortrix
RT contortrix).";
RL Arch. Biochem. Biophys. 289:197-207(1991).
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1209 MW; 7CA02D1D41E8772B CRC64;

Query Match 45.8%; Score 27; DB 13; Length 11;
Best Local Similarity 71.4%; Pred. No. 1.4e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```
Qy          6 QLMHNLG 12
              :| ||||
Db          4 ELGHNLG 10
```

RESULT 2
P82081
ID P82081 PRELIMINARY; PRT; 12 AA.
AC P82081;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

```
DT   01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE   DYNASTIN 3.
OS   Limnodynastes terraereginae (Northen banjo frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Myobatrachidae;
OC   Limnodynastinae; Limnodynastes.
OX   NCBI_TaxID=104894;
RN   [1]
RP   SEQUENCE, AND MASS SPECTROMETRY.
RC   TISSUE=TIBIAL GLAND;
RA   Raftery M.J., Bradford A.M., Bowie J.H., Wallace J.C., Tyler M.J.;
RT   "Peptides from Australian frogs. The structure of the dynastins from
RT   the banjo frogs Limnodynastes interioras, Limnodynastes dumerilii and
RT   Limnodynastes terraereginae.";
RL   Aust. J. Chem. 46:833-842(1993).
CC   -!- MASS SPECTROMETRY: MW=1236; METHOD=FAB.
SQ   SEQUENCE   12 AA;  1236 MW;  147AA70FDF472724 CRC64;

  Query Match             39.0%;  Score 23;  DB 13;  Length 12;
  Best Local Similarity   66.7%;  Pred. No. 1e+03;
  Matches    4;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 LMHNLG 12
              |::|||
Db          6 LLNNLG 11


RESULT 3
P82082
ID   P82082      PRELIMINARY;      PRT;     8 AA.
AC   P82082;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE   DYNASTIN 4.
OS   Limnodynastes salmini (Salmin's-striped frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Myobatrachidae;
OC   Limnodynastinae; Limnodynastes.
OX   NCBI_TaxID=39404;
RN   [1]
RP   SEQUENCE, AND MASS SPECTROMETRY.
RC   TISSUE=SKIN SECRETION;
RA   Bradford A.M., Raftery M.J., Bowie J.H., Wallace J.C., Tyler M.J.;
RT   "Peptides from Australian frogs. The structure of the dynastins from
RT   Limnodynastes salmini and Fletcherin from Limnodynastes fletcheri.";
RL   Aust. J. Chem. 46:1235-1244(1993).
CC   -!- MASS SPECTROMETRY: MW=772; METHOD=FAB.
SQ   SEQUENCE   8 AA;  772 MW;  7B58772455A2C728 CRC64;

  Query Match             33.9%;  Score 20;  DB 13;  Length 8;
  Best Local Similarity   66.7%;  Pred. No. 1e+06;
  Matches    4;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 LMHNLG 12
              |: |||
Db          2 LVSNLG 7


RESULT 4
P82083
ID   P82083      PRELIMINARY;      PRT;     8 AA.
AC   P82083;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE   DYNASTIN 5.
OS   Limnodynastes salmini (Salmin's-striped frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Myobatrachidae;
OC   Limnodynastinae; Limnodynastes.
OX   NCBI_TaxID=39404;
RN   [1]
RP   SEQUENCE, AND MASS SPECTROMETRY.
RC   TISSUE=SKIN SECRETION;
RA   Bradford A.M., Raftery M.J., Bowie J.H., Wallace J.C., Tyler M.J.;
RT   "Peptides from Australian frogs. The structure of the dynastins from
RT   Limnodynastes salmini and Fletcherin from Limnodynastes fletcheri.";
RL   Aust. J. Chem. 46:1235-1244(1993).
CC   -!- MASS SPECTROMETRY: MW=786; METHOD=FAB.
SQ   SEQUENCE   8 AA;  786 MW;  7B58772455B05728 CRC64;

  Query Match             33.9%;  Score 20;  DB 13;  Length 8;
  Best Local Similarity   66.7%;  Pred. No. 1e+06;
  Matches    4;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 LMHNLG 12
              |: |||
Db          2 LISNLG 7


RESULT 5
P82085
ID   P82085      PRELIMINARY;      PRT;     12 AA.
AC   P82085;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE   DYNASTIN 7.
OS   Limnodynastes salmini (Salmin's-striped frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Myobatrachidae;
OC   Limnodynastinae; Limnodynastes.
OX   NCBI_TaxID=39404;
RN   [1]
RP   SEQUENCE, AND MASS SPECTROMETRY.
RC   TISSUE=SKIN SECRETION;
RA   Bradford A.M., Raftery M.J., Bowie J.H., Wallace J.C., Tyler M.J.;
RT   "Peptides from Australian frogs. The structure of the dynastins from
RT   Limnodynastes salmini and Fletcherin from Limnodynastes fletcheri.";
RL   Aust. J. Chem. 46:1235-1244(1993).
CC   -!- MASS SPECTROMETRY: MW=1114; METHOD=FAB.
SQ   SEQUENCE   12 AA;  1114 MW;  3AB5A976CAA72728 CRC64;

  Query Match             33.9%;  Score 20;  DB 13;  Length 12;
  Best Local Similarity   66.7%;  Pred. No. 4.2e+03;
  Matches    4;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 LMHNLG 12
              |: |||
Db          6 LLTNLG 11


RESULT 6
Q34909
ID   Q34909      PRELIMINARY;      PRT;     8 AA.
AC   Q34909;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Cytochrome b (Fragment).
OS   Locusta migratoria (Migratory locust).
OG   Mitochondrion.
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
OC   Acridoidea; Acrididae; Oedipodinae; Locusta.
OX   NCBI_TaxID=7004;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=88223478; PubMed=2836084;
RA   McCracken A., Uhlenbusch I., Gellissen G.;
RT   "Structure of the cloned Locusta migratoria mitochondrial genome:
RT   restriction mapping and sequence of its ND-1(URF-1) gene.";
RL   Curr. Genet. 11:625-630(1987).
DR   EMBL; X05286; CAA28905.1; -.
DR   GO; GO:0005739; C:mitochondrion; IEA.
```

```
KW   Mitochondrion.
FT   NON_TER       1      1
FT   NON_TER       8      8
SQ   SEQUENCE   8 AA;  1019 MW;  F8E33723304B45B6 CRC64;

  Query Match             32.2%;  Score 19;  DB 8;  Length 8;
  Best Local Similarity   50.0%;  Pred. No. 1e+06;
  Matches    4;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 VSEIQLMH 9
              :| |:| |
Db          1 MSYIKLKH 8


RESULT 7
O92766
ID   O92766      PRELIMINARY;      PRT;     9 AA.
AC   O92766;
DT   01-NOV-1998 (TrEMBLrel. 08, Created)
DT   01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT   01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE   Fusion protein (Fragment).
GN   F.
OS   Canine distemper virus.
OC   Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC   Paramyxoviridae; Paramyxovirinae; Morbillivirus.
OX   NCBI_TaxID=11232;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Dog #5526/89;
RA   Liermann H., Harder T., Haas L.;
RT   "Genetic analysis of the central untranslated genome region and the
RT   proximal coding part of the F gene of wild-type and vaccine distemper
RT   morbilliviruses.";
RL   Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF026237; AAC09167.1; -.
FT   NON_TER       9      9
SQ   SEQUENCE   9 AA;  1011 MW;  F281732760533441 CRC64;

  Query Match             32.2%;  Score 19;  DB 12;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 1e+06;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 MHN 10
              |||
Db          1 MHN 3


RESULT 8
O71066
ID   O71066      PRELIMINARY;      PRT;     9 AA.
AC   O71066;
DT   01-AUG-1998 (TrEMBLrel. 07, Created)
DT   01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   Fusion protein (Fragment).
GN   F.
OS   Canine distemper virus.
OC   Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC   Paramyxoviridae; Paramyxovirinae; Morbillivirus.
OX   NCBI_TaxID=11232;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Dog #10757/96;
RA   Liermann H., Harder T., Haas L.;
RT   "Genetic analysis of the central untranslated genome region and the
RT   proximal coding part of the F gene of wild-type and vaccine distemper
RT   morbilliviruses.";
RL   Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF026234; AAC09164.1; -.
FT   NON_TER       9      9
SQ   SEQUENCE   9 AA;  1124 MW;  F29D045760440441 CRC64;

  Query Match             32.2%;  Score 19;  DB 12;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 1e+06;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 MHN 10
              |||
Db          1 MHN 3


RESULT 9
Q40659
ID   Q40659      PRELIMINARY;      PRT;     8 AA.
AC   Q40659;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE   Alpha-amylase (Fragment).
OS   Oryza sativa (Rice).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC   Ehrhartoideae; Oryzeae; Oryza.
OX   NCBI_TaxID=4530;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91078641; PubMed=2258052;
RA   Kumagai M.H., Shah M., Terashima M., Vrkljan Z., Whitaker J.R.,
RA   Rodriquez R.L.;
RT   "Expression and secretion of rice alpha-amylase by saccharomycers
RT   cerevisiae.";
RL   Gene 94:209-216(1990).
DR   EMBL; M62916; AAA33892.1; -.
DR   Gramene; Q40659; -.
FT   NON_TER       8      8
SQ   SEQUENCE   8 AA;  948 MW;  EBC694444732D6D6 CRC64;

  Query Match             30.5%;  Score 18;  DB 10;  Length 8;
  Best Local Similarity   28.6%;  Pred. No. 1e+06;
  Matches    2;  Conservative    5;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 IQLMHNL 11
              :|:::|:
Db          1 MQVLNNM 7


RESULT 10
Q9PXC3
ID   Q9PXC3      PRELIMINARY;      PRT;    10 AA.
AC   Q9PXC3;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   E antigen P20E (Fragment).
OS   Hepatitis B virus.
OC   Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX   NCBI_TaxID=10407;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=92013147; PubMed=1717588;
RA   Takahashi K., Kishimoto S., Ohori K., Yoshizawa H., Machida A.,
RA   Ohnuma H., Tsuda F., Munekata E., Miyakawa Y., Mayumi M.;
RT   "Molecular heterogeneity of e antigen polypeptides in sera from
RT   carriers of hepatitis B virus.";
RL   J. Immunol. 147:3156-3160(1991).
DR   PIR; B46453; B46453.
FT   NON_TER      10     10
SQ   SEQUENCE   10 AA;  1238 MW;  485A6E3AE721E9C7 CRC64;

  Query Match             30.5%;  Score 18;  DB 12;  Length 10;
  Best Local Similarity   60.0%;  Pred. No. 8.9e+03;
  Matches    3;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          5 IQLMH 9
              :|| |
```

```
Db          1 MQLFH 5


RESULT 11
Q23876
ID   Q23876      PRELIMINARY;      PRT;    11 AA.
AC   Q23876;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE   Actin 4.
OS   Dictyostelium discoideum (Slime mold).
OC   Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
OX   NCBI_TaxID=44689;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=82260445; PubMed=6286214;
RA   McKeown M., Firtel R.A.;
RT   "Actin multigene family of Dictyostelium.";
RL   Cold Spring Harb. Symp. Quant. Biol. 46:495-505(1982).
DR   EMBL; K02957; AAA33150.1; -.
DR   EMBL; K02956; AAA33150.1; JOINED.
SQ   SEQUENCE   11 AA;  1205 MW;  728B4C14C6C2CAAB CRC64;

  Query Match             30.5%;  Score 18;  DB 5;  Length 11;
  Best Local Similarity   28.6%;  Pred. No. 9.9e+03;
  Matches    2;  Conservative    4;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 EIQLMHN 10
              ::|. ::|
Db          5 DVQALNN 11


RESULT 12
Q85631
ID   Q85631      PRELIMINARY;      PRT;    12 AA.
AC   Q85631;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   MH2, proviral DNA, myc to 3' LTR (Fragment).
OS   Avian carcinoma virus.
OC   Viruses; Retroid viruses; Retroviridae; Alpharetrovirus.
OX   NCBI_TaxID=11958;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=85033920; PubMed=6092695;
RA   Sutrave P., Jansen H.W., Bister K., Rapp U.R.;
RT   "3'-terminal region of avian carcinoma virus MH2 shares sequence
RT   elements with avian sarcoma viruses Y73 and SR-A.";
RL   J. Virol. 52:703-705(1984).
DR   EMBL; K03100; AAA42388.1; -.
FT   NON_TER       1      1
SQ   SEQUENCE   12 AA;  1466 MW;  72E4B884F30736DB CRC64;

  Query Match             30.5%;  Score 18;  DB 15;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+04;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          9 HNL 11
              |||
Db          2 HNL 4


RESULT 13
Q28742
ID   Q28742      PRELIMINARY;      PRT;     7 AA.
AC   Q28742;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Alpha-myosin heavy chain (Fragment).
OS   Oryctolagus cuniculus (Rabbit).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX   NCBI_TaxID=9986;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=84221901; PubMed=6328491;
RA   Friedman D.J., Umeda P.K., Sinha A.M., Hsu H.-J., Jokovcic S.,
RA   Rabinowitz M.;
RT   "Characterization of genomic clones specifying rabbit alpha- and beta-
RT   ventricular myosin heavy chains.";
RL   Proc. Natl. Acad. Sci. U.S.A. 81:3044-3048(1984).
DR   EMBL; K01698; AAA31415.1; -.
DR   PIR; I46868; I46868.
FT   NON_TER       1      1
SQ   SEQUENCE   7 AA;  916 MW;  6B1B1AA1E69326B0 CRC64;

  Query Match             28.8%;  Score 17;  DB 6;  Length 7;
  Best Local Similarity   60.0%;  Pred. No. 1e+06;
  Matches    3;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          6 QLMHN 10
              | ||:
Db          1 QKMHD 5


RESULT 14
Q15891
ID   Q15891      PRELIMINARY;      PRT;     9 AA.
AC   Q15891;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   (Clone XP2E8B) (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Placenta;
RA   Lee C.-C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M.,
RA   Coolbaugh M.I., Chinault C.A., Baldini A., Lindsay E.A., Zhao Z.-Y.,
RA   Caskey C.T.H.;
RT   "Isolation of chromosome-specific genes by reciprocal probing of
RT   arrayed cDNAs and cosmid libraries.";
RL   Hum. Mol. Genet. 0:0-0(1995).
DR   EMBL; L32131; AAA73881.1; -.
FT   NON_TER       1      1
FT   NON_TER       9      9
SQ   SEQUENCE   9 AA;  1030 MW;  E56635A1A33686D1 CRC64;

  Query Match             28.8%;  Score 17;  DB 4;  Length 9;
  Best Local Similarity   44.4%;  Pred. No. 1e+06;
  Matches    4;  Conservative    2;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          4 EIQLMHNLG 12
              | |:  :||
Db          1 EHQMKTSLG 9


RESULT 15
Q9GD12
ID   Q9GD12      PRELIMINARY;      PRT;     9 AA.
AC   Q9GD12;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Ribosomal protein S16 (Fragment).
GN   RPS16.
OS   Linospadix monostachya.
OG   Chloroplast.
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; Liliopsida; Arecaceae; Arecoideae;
```

```
OC   Areceae; Linospadicinae; Linospadix.
OX   NCBI_TaxID=131282;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Leaf;
RA   Asmussen C.B., Chase M.W.;
RT   "Coding and noncoding plastid DNA in palm systematics.";
RL   Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AJ404941; CAC17917.1; -.
DR   GO; GO:0009507; C:chloroplast; IEA.
KW   Chloroplast.
FT   NON_TER       1      1
FT   NON_TER       9      9
SQ   SEQUENCE   9 AA;  1106 MW;  1B9236C2C0441B50 CRC64;

  Query Match             28.8%;  Score 17;  DB 8;  Length 9;
  Best Local Similarity   75.0%;  Pred. No. 1e+06;
  Matches    3;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 IQLM 8
              :|||
Db          6 VQLM 9


Search completed: September  5, 2004, 09:37:00
Job time : 27.5 secs
```

OM protein - protein search, using sw model

Run on: September 5, 2004, 09:26:47 ; Search time 36.5 Seconds
(without alignments)
92.892 Million cell updates/sec

Title: US-09-730-174A-5
Perfect score: 59
Sequence: 1 AVSEIQLMHNLG 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 368311

Minimum DB seq length: 0
Maximum DB seq length: 12

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	53	89.8	11	3	AAY96968	Aay96968 Parathyro
2	50	84.7	11	6	ABG72607	Abg72607 Parathyro
3	50	84.7	12	6	ABG72608	Abg72608 Parathyro
4	46	78.0	10	2	AAR91644	Aar91644 Human par
5	46	78.0	10	3	AAY68767	Aay68767 Amino aci
6	46	78.0	10	4	AAB86219	Aab86219 Human par
7	46	78.0	10	6	ABR44166	Abr44166 Human par
8	45	76.3	9	4	AAB86225	Aab86225 Human par
9	43.5	73.7	11	2	AAY50600	Aay50600 Resin bou
10	43	72.9	9	3	AAB01862	Aab01862 PTH(1-14)
11	43	72.9	9	3	AAY96966	Aay96966 Parathyro
12	40	67.8	9	2	AAR91645	Aar91645 Human par
13	40	67.8	9	3	AAB01863	Aab01863 PTH(1-14)
14	40	67.8	9	3	AAY96981	Aay96981 Parathyro
15	40	67.8	9	4	AAB86220	Aab86220 Human par
16	40	67.8	10	4	AAB96932	Aab96932 Rat parat
17	40	67.8	11	4	AAB96931	Aab96931 Rat parat
18	40	67.8	11	4	AAB96915	Aab96915 Parathyro
19	40	67.8	11	4	AAB84770	Aab84770 Parathyro
20	40	67.8	12	4	AAB96914	Aab96914 Parathyro
21	40	67.8	12	4	AAB84769	Aab84769 Parathyro
22	38	64.4	12	2	AAW45785	Aaw45785 Parathyro
23	35	59.3	10	6	ABP71484	Abp71484 Parathyro
24	35	59.3	11	1	AAP82547	Aap82547 (Asn10, T
25	35	59.3	11	4	AAB96892	Aab96892 Rat parat
26	35	59.3	11	6	ABP71485	Abp71485 Parathyro
27	35	59.3	11	6	ABP71483	Abp71483 Parathyro
28	35	59.3	12	4	AAB96891	Aab96891 Rat parat
29	35	59.3	12	6	ABP71482	Abp71482 Parathyro
30	33	55.9	9	3	AAB01864	Aab01864 PTH(1-14)
31	33	55.9	9	3	AAY78849	Aay78849 Parathyro
32	33	55.9	9	3	AAY97062	Aay97062 PTH-rP N-
33	32	54.2	8	2	AAR91646	Aar91646 Human par
34	32	54.2	8	3	AAB07467	Aab07467 Antigenic
35	32	54.2	8	4	AAB86221	Aab86221 Human par
36	30	50.8	9	3	AAB01866	Aab01866 PTH(1-14)
37	27	45.8	7	2	AAR91647	Aar91647 Human par
38	27	45.8	7	4	AAB86222	Aab86222 Human par
39	27	45.8	10	5	ABG98580	Abg98580 F protein
40	27	45.8	10	5	ABG98582	Abg98582 F protein
41	27	45.8	10	5	ABG98581	Abg98581 F protein
42	27	45.8	11	4	ABU54029	Abu54029 Human DNA
43	27	45.8	12	2	AAR89301	Aar89301 Japanese
44	27	45.8	12	2	AAR64520	Aar64520 RF-2 pept
45	27	45.8	12	3	AAB21270	Aab21270 Fertilin

ALIGNMENTS

RESULT 1
AAY96968
ID AAY96968 standard; peptide; 11 AA.
XX
AC AAY96968;
XX
DT 31-OCT-2000 (first entry)
XX
DE Parathyroid hormone N-terminal signaling domain (residues 1-11).
XX
KW PTH; parathyroid hormone; N-terminal; signaling domain; bone mass;
KW bone reformation; resorption; remodeling; tether1; osteoporosis.
XX
OS Homo sapiens.
XX
PN WO200039278-A2.
XX
PD 06-JUL-2000.
XX
PF 30-DEC-1999; 99WO-US031108.
XX
PR 31-DEC-1998; 98US-0114577P.
XX
PA (GARD/) GARDELLA T J.
PA (KRON/) KRONENBERG H M.
PA (POTT/) POTTS J T.
PA (JUEP/) JUEPPNER H.
XX
PI Gardella TJ, Kronenberg HM, Potts JT, Jueppner H;
XX
DR WPI; 2000-452384/39.
XX
PT New compound comprising an amino terminal signaling functional domain
PT linked to a carboxy-terminal binding portion of parathyroid hormone for
PT treating mammalian conditions characterized by decreases in bone mass.
XX
PS Claim 4; Page 92; 119pp; English.
XX
CC Compounds of the structure or formula S-(L)_n-B, R_1-S-(L)_n-R or S-(L)_n
CC -R, are new. S is an amino terminal signaling functional domain of
CC parathyroid hormone (PTH); L is a linker molecule present n times (where
CC n is a positive integer 1-10 (preferably 4)); B is a C-terminal binding
CC portion of PTH(1-34) or a PTH-related protein (PTH-rP) (1-34); R_1 is the
CC PTH-1 receptor signal sequence; and R is (a portion of) PTH-1 receptor
CC sequence. The new compounds are used for treating mammalian conditions
CC characterized by decreases in bone mass, determining rates of bone
CC reformation, bone resorption and/or bone remodeling, treating diseases
CC and disorders associated with decreased tether1 activity, increasing cAMP

CC in a mammalian cell having PTH-1 receptors, or screening for a peptide or
CC non-peptide PTH (claimed). The new compound can be administered by
CC inhalation unlike the large native PTH or PTHrP which avoids the need for
CC regular injections to treat osteoporosis
XX
SQ Sequence 11 AA;

Query Match 89.8%; Score 53; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0034;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AVSEIQLMHNL 11
||||||||||||
Db 1 AVSEIQLMHNL 11

RESULT 2
ABG72607
ID ABG72607 standard; peptide; 11 AA.
XX
AC ABG72607;
XX
DT 11-FEB-2003 (first entry)
XX
DE Parathyroid hormone antigenic peptide 2-12.
XX
KW Human; parathyroid hormone; antigen; hypercalcaemia; osteoporosis;
KW primary hyperparathyroidism; mouse; rat; bovine; porcine; canine.
XX
OS Homo sapiens.
OS Mus sp.
OS Rattus sp.
OS Bos taurus.
OS Sus scrofa.
OS Canis familiaris.
XX
FH Key Location/Qualifiers
FT Misc-difference 6
FT /label= Leu, Phe
XX
PN US2002110871-A1.
XX
PD 15-AUG-2002.
XX
PF 05-DEC-2000; 2000US-00730174.
XX
PR 05-DEC-2000; 2000US-00730174.
XX
PA (ZAHR/) ZAHRADNIK R J.
PA (LAVI/) LAVIGNE J R.
XX
PI Zahradnik RJ, Lavigne JR;
XX
DR WPI; 2003-066685/06.
XX
PT New parathyroid hormone (PTH) antigenic peptide inducing the formation
PT and isolation of antibodies having an affinity to it, useful for
PT determining bioactive PTH levels in serum, plasma and/or cell culture
PT media.
XX
PS Claim 1; Page 5; 11pp; English.
XX
CC The invention relates to a new antigenic peptide for inducing the
CC formation and isolation of antibodies having an affinity to it, being
CC formed from the N-terminus of parathyroid hormone (PTH). Also included
CC are; (1) a method for producing antibodies useful in the determination of
CC PTH levels in a biological sample comprising: (a) providing at least one
CC first peptide antigen comprising a peptide fragment of PTH; (b)
CC administering the first peptide antigen to a host animal to induce
CC antibody production; (c) monitoring the antibody titre produced; (d)
CC isolating antisera produced in the host animal; and (e) selecting
CC antisera from the isolated antisera produced in the host that is capable
CC of binding to a second peptide antigen; (2) an antibody (ab) produced by
CC the method; and (3) test kits and analytical procedures used for the
CC determination of bioactive intact PTH utilising (ab). The methods and
CC compositions of the present invention are useful for determining
CC bioactive intact PTH levels in serum, plasma and/or cell culture media.
CC The antigens, antibodies and methods of the present invention, as
CC compared to prior art, have the particular advantages of possessing
CC greater affinity for PTH, and in particular, are designed to have a novel
CC recognition for amino acid residues extending beyond the first N-terminal
CC PTH residue, and further have negligible cross-reactivity with the large
CC non-molecular forms of PTH. PTH levels are an important parameter in
CC patients suffering from hypercalcaemia, osteoporosis and primary
CC hyperparathyroidism. The present sequence represents a PTH antigenic
CC peptide representing amino acids 2-12 of human, mouse, rat, porcine,
CC canine and bovine PTH
XX
SQ Sequence 11 AA;

Query Match 84.7%; Score 50; DB 6; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.012;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 VSEIQLMHNLG 12
||||| |||||
Db 1 VSEIQXMHNLG 11

RESULT 3
ABG72608
ID ABG72608 standard; peptide; 12 AA.
XX
AC ABG72608;
XX
DT 11-FEB-2003 (first entry)
XX
DE Parathyroid hormone antigenic peptide 1-12.
XX
KW Human; parathyroid hormone; antigen; hypercalcaemia; osteoporosis;
KW primary hyperparathyroidism; mouse; rat; bovine; porcine; canine.
XX
OS Homo sapiens.
OS Mus sp.
OS Rattus sp.
OS Bos taurus.
OS Sus scrofa.
OS Canis familiaris.
XX
FH Key Location/Qualifiers
FT Misc-difference 1
FT /label= Ser, Ala
FT Misc-difference 7
FT /label= Leu, Phe
XX
PN US2002110871-A1.
XX
PD 15-AUG-2002.
XX
PF 05-DEC-2000; 2000US-00730174.
XX
PR 05-DEC-2000; 2000US-00730174.
XX
PA (ZAHR/) ZAHRADNIK R J.
PA (LAVI/) LAVIGNE J R.
XX
PI Zahradnik RJ, Lavigne JR;
XX
DR WPI; 2003-066685/06.
XX
PT New parathyroid hormone (PTH) antigenic peptide inducing the formation
PT and isolation of antibodies having an affinity to it, useful for
PT determining bioactive PTH levels in serum, plasma and/or cell culture
PT media.
XX
PS Claim 2; Page 5; 11pp; English.

XX
CC The invention relates to a new antigenic peptide for inducing the
CC formation and isolation of antibodies having an affinity to it, being
CC formed from the N-terminus of parathyroid hormone (PTH). Also included
CC are; (1) a method for producing antibodies useful in the determination of
CC PTH levels in a biological sample comprising: (a) providing at least one
CC first peptide antigen comprising a peptide fragment of PTH; (b)
CC administering the first peptide antigen to a host animal to induce
CC antibody production; (c) monitoring the antibody titre produced; (d)
CC isolating antisera produced in the host animal; and (e) selecting
CC antisera from the isolated antisera produced in the host that is capable
CC of binding to a second peptide antigen; (2) an antibody (ab) produced by
CC the method; and (3) test kits and analytical procedures used for the
CC determination of bioactive intact PTH utilising (ab). The methods and
CC compositions of the present invention are useful for determining
CC bioactive intact PTH levels in serum, plasma and/or cell culture media.
CC The antigens, antibodies and methods of the present invention, as
CC compared to prior art, have the particular advantages of possessing
CC greater affinity for PTH, and in particular, are designed to have a novel
CC recognition for amino acid residues extending beyond the first N-terminal
CC PTH residue, and further have negligible cross-reactivity with the large
CC non-molecular forms of PTH. PTH levels are an important parameter in
CC patients suffering from hypercalcaemia, osteoporosis and primary
CC hyperparathyroidism. The present sequence represents a PTH antigenic
CC peptide representing amino acids 1-12 of human, mouse, rat, porcine,
CC canine and bovine PTH
XX
SQ Sequence 12 AA;

Query Match 84.7%; Score 50; DB 6; Length 12;
Best Local Similarity 90.9%; Pred. No. 0.014;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 VSEIQLMHNLG 12
||||| |||||
Db 2 VSEIQXMHNLG 12

RESULT 4
AAR91644
ID AAR91644 standard; peptide; 10 AA.
XX
AC AAR91644;
XX
DT 06-NOV-1996 (first entry)
XX
DE Human parathyroid hormone antigenic peptide hPTH 1-10.
XX
KW Human parathyroid hormone; hPTH; antigen; alpha-helix; immunogen;
KW diagnosis; active hPTH 1-37.
XX
OS Synthetic.
XX
PN DE4434551-A1.
XX
PD 04-APR-1996.
XX
PF 28-SEP-1994; 94DE-04434551.
XX
PR 28-SEP-1994; 94DE-04434551.
XX
PA (FORS/) FORSSMANN W.
XX
PI Adermann K, Forssmann W, Hock D, Maegerlein M;
XX
DR WPI; 1996-180391/19.
XX
PT New antigenic peptide(s) from human parathyroid hormone - and antibodies
PT generated using them, able to distinguish between active and inactive
PT forms of the hormone.
XX
PS Claim 2; Page 4; 5pp; German.
XX
CC The present sequence is a specific example of claimed immunogenic
CC peptides having a sequence from hPTH(1-37) which includes the N- or C-
CC terminal alpha-helical region and/or the non-structured region of the
CC hormone. Antibodies and their binding fragments generated by injecting an
CC animal with the peptides are useful as diagnostic reagents for
CC determination of biologically active hPTH(1-37)
XX
SQ Sequence 10 AA;

Query Match 78.0%; Score 46; DB 2; Length 10;
Best Local Similarity 90.0%; Pred. No. 0.061;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AVSEIQLMHN 10
:|||||||||
Db 1 SVSEIQLMHN 10

RESULT 5
AAY68767
ID AAY68767 standard; peptide; 10 AA.
XX
AC AAY68767;
XX
DT 05-MAY-2000 (first entry)
XX
DE Amino acids 1-10 of a parathyroid hormone (pTH).
XX
KW Parathyroid hormone; lipolysis; cosmetic; dermatological; skin care;
KW slimming treatment; cellulite; skin firming.
XX
OS Unidentified.
XX
PN WO200004047-A1.
XX
PD 27-JAN-2000.
XX
PF 07-JUL-1999; 99WO-FR001687.
XX
PR 17-JUL-1998; 98FR-00009193.
XX
PA (SEDE-) SEDERMA.
XX
PI Lintner K;
XX
DR WPI; 2000-171243/15.
XX
PT New parathyroid hormone fragment peptides, used as lipolysis stimulants
PT in topically applied cosmetic compositions for slimming treatment of
PT excessive weight in hips and thighs.
XX
PS Claim 1; Page 8; 18pp; French.
XX
CC The present sequence represents a parathyroid hormone (pTH) fragment,
CC comprising amino acids 1-10. Parathyroid hormone fragments of the
CC invention have lipolysis stimulating activity (especially when topically
CC administered). The lipolytic activity of the peptides is enhanced when
CC they are chemically modified to increase their lipophilicity. The
CC peptides are used in cosmetic or dermatological compositions for skin
CC care. They are especially used for slimming treatment of excessive weight
CC in the thighs and hips, in the treatment of cellulite and for skin
CC firming
XX
SQ Sequence 10 AA;

Query Match 78.0%; Score 46; DB 3; Length 10;
Best Local Similarity 90.0%; Pred. No. 0.061;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AVSEIQLMHN 10
:|||||||||
Db 1 SVSEIQLMHN 10

RESULT 6
AAB86219
ID AAB86219 standard; peptide; 10 AA.
XX
AC AAB86219;
XX
DT 03-SEP-2001 (first entry)
XX
DE Human parathyroid hormone immunogenic peptide SEQ ID 1.
XX
KW Parathyroid hormone; hPTH; immunogenic peptide; human; epitope;
KW diagnosis; calcium-metabolism disorder; osteopathy; antagonist;
KW hypo-parathyroidism; hyper-parathyroidism.
XX
OS Homo sapiens.
XX
PN DE19961350-A1.
XX
PD 21-JUN-2001.
XX
PF 17-DEC-1999; 99DE-01061350.
XX
PR 17-DEC-1999; 99DE-01061350.
XX
PA (IMMU-) IMMUNDIAGNOSTIK AG.
XX
PI Armbruster FP;
XX
DR WPI; 2001-376318/40.
XX
PT Determining the content of physiologically active parathyroid hormone,
PT useful in diagnosis of calcium-metabolism disorders, using two antibodies
PT reactive with different epitopes.
XX
PS Disclosure; Page 3; 10pp; German.
XX
CC This invention describes a novel method for determining (M1) the content
CC of active parathyroid hormone (A) by treating a sample with (i) antibody
CC (Ab1) that recognizes the epitope formed by amino acids (aa) 1-3 of (A),
CC and including the N-terminal residue and (ii) antibody (Ab2) that
CC recognizes an epitope within the receptor-binding site of (A). The number
CC of molecules that react with both antibodies is determined and used to
CC calculate the content of physiologically active (A). The method is used
CC for diagnosis of calcium-metabolism disorders, osteopathy, or hypo- or
CC hyper-parathyroidism. The method (unlike known assays) recognizes that
CC (i) some fragments of (A) shorter than the complete (84 aa) peptide are
CC active and (ii) that apparently intact peptide may be biologically
CC inactive, and also takes into account the fact that some fragments of (A)
CC are antagonistic (these have the receptor-binding site but lack the N-
CC terminus). It thus provides a true measure of the content of
CC physiologically active (A); contrast methods that measure intact peptide
CC and its 1-37 fragment which may produce falsely high values. This
CC sequence represents a peptide fragment used to illustrate the method of
CC the invention
XX
SQ Sequence 10 AA;

Query Match 78.0%; Score 46; DB 4; Length 10;
Best Local Similarity 90.0%; Pred. No. 0.061;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AVSEIQLMHN 10
:|||||||||
Db 1 SVSEIQLMHN 10

RESULT 7
ABR44166
ID ABR44166 standard; peptide; 10 AA.
XX
AC ABR44166;
XX
DT 04-AUG-2003 (first entry)
XX
DE Human parathyroid hormone (hPTH) fragment (residues 1-10).
XX
KW Fusion peptide; tat; hPTHDP; parathyroid hormone; skin; cosmetic;
KW lipolysis; human; hPTH.
XX
OS Homo sapiens.
XX
PN WO2003035697-A1.
XX
PD 01-MAY-2003.
XX
PF 06-MAY-2002; 2002WO-KR000835.
XX
PR 27-SEP-2001; 2001KR-00060245.
PR 15-MAR-2002; 2002KR-00014062.
XX
PA (GLDS) LG HOUSEHOLD & HEALTH CARE LTD.
XX
PI Song Y, Kang N, Park S, Cho W, Kang S, Lee Y, Lim J, Min H;
PI Chang M;
XX
DR WPI; 2003-468288/44.
XX
PT Novel fusion peptide comprising self cell-penetrating Tat peptide bound
PT to human parathyroid hormone-derived peptide, useful as component of skin
PT slimming cosmetic composition.
XX
PS Claim 5; Page 6; 32pp; English.
XX
CC The invention relates to a fusion peptide (Tat-hPTHDP), where self cell-
CC penetrating Tat peptide is bound to human parathyroid hormone-derived
CC peptide (hPTHDP). The fusion peptide is useful as a component of skin
CC slimming cosmetic composition. The fusion peptide does not cause
CC irritation, easily and safely penetrates into integument and endothelium,
CC does not cause skin disease and has superior lipolysis effects, and is
CC durable. The present sequence represents a human parathyroid hormone
CC (hPTH) fragment that can be used to construct the fusion peptide
XX
SQ Sequence 10 AA;

Query Match 78.0%; Score 46; DB 6; Length 10;
Best Local Similarity 90.0%; Pred. No. 0.061;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AVSEIQLMHN 10
:|||||||||
Db 1 SVSEIQLMHN 10

RESULT 8
AAB86225
ID AAB86225 standard; peptide; 9 AA.
XX
AC AAB86225;
XX
DT 03-SEP-2001 (first entry)
XX
DE Human parathyroid hormone immunogenic peptide SEQ ID 7.
XX
KW Parathyroid hormone; hPTH; immunogenic peptide; human; epitope;
KW diagnosis; calcium-metabolism disorder; osteopathy; antagonist;
KW hypo-parathyroidism; hyper-parathyroidism.
XX
OS Homo sapiens.
XX
PN DE19961350-A1.
XX
PD 21-JUN-2001.
XX
PF 17-DEC-1999; 99DE-01061350.
XX

PR 17-DEC-1999; 99DE-01061350.
XX
PA (IMMU-) IMMUNDIAGNOSTIK AG.
XX
PI Armbruster FP;
XX
DR WPI; 2001-376318/40.
XX
PT Determining the content of physiologically active parathyroid hormone,
PT useful in diagnosis of calcium-metabolism disorders, using two antibodies
PT reactive with different epitopes.
XX
PS Disclosure; Page 3; 10pp; German.
XX
CC This invention describes a novel method for determining (M1) the content
CC of active parathyroid hormone (A) by treating a sample with (i) antibody
CC (Ab1) that recognizes the epitope formed by amino acids (aa) 1-3 of (A),
CC and including the N-terminal residue and (ii) antibody (Ab2) that
CC recognizes an epitope within the receptor-binding site of (A). The number
CC of molecules that react with both antibodies is determined and used to
CC calculate the content of physiologically active (A). The method is used
CC for diagnosis of calcium-metabolism disorders, osteopathy, or hypo- or
CC hyper-parathyroidism. The method (unlike known assays) recognizes that
CC (i) some fragments of (A) shorter than the complete (84 aa) peptide are
CC active and (ii) that apparently intact peptide may be biologically
CC inactive, and also takes into account the fact that some fragments of (A)
CC are antagonistic (these have the receptor-binding site but lack the N-
CC terminus). It thus provides a true measure of the content of
CC physiologically active (A); contrast methods that measure intact peptide
CC and its 1-37 fragment which may produce falsely high values. This
CC sequence represents a peptide fragment used to illustrate the method of
CC the invention
XX
SQ Sequence 9 AA;

Query Match 76.3%; Score 45; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.4e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VSEIQLMHN 10
|||||||||
Db 1 VSEIQLMHN 9

RESULT 9
AAY50600
ID AAY50600 standard; peptide; 11 AA.
XX
AC AAY50600;
XX
DT 09-FEB-2000 (first entry)
XX
DE Resin bound cyclic peptide 33.
XX
KW Cyclic peptide; resin bound; parathyroid hormone; osteopathic; disease;
KW hypotensive; PTH receptor; treatment; hyper-calcemia; hypo-calcemia;
KW osteoporosis; osteopenia; hyper-parathyroidism; hypo-parathyroidism;
KW Cushing's syndrome; renal failure; hypertension; bone fracture repair.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 1
FT /note= "FMOC-Ala"
FT Misc-difference 3
FT /note= "Ser(OtBu)"
FT Misc-difference 4
FT /note= "Glu(OtBu)"
FT Misc-difference 6
FT /note= "Gln(Trt)"
FT Misc-difference 9
FT /note= "His(Trt)"
FT Misc-difference 10
FT /note= "Asn(Trt)"
XX
PN WO9952933-A1.
XX
PD 21-OCT-1999.
XX
PF 15-APR-1999; 99WO-US008435.
XX
PR 15-APR-1998; 98US-0081897P.
XX
PA (RHON) RHONE-POULENC RORER PHARM INC.
XX
PI Sledeski AW, Mencel JJ;
XX
DR WPI; 1999-633822/54.
XX
PT Convergent synthesis of peptides for treating e.g. bone disorders.
XX
PS Disclosure; Page 75; 85pp; English.
XX
CC This invention describes a novel method for the preparation of peptides
CC (II) that contain both cyclic and linear peptide fragments comprises
CC sequential reaction of a resin-bound linear fragment with the cyclic
CC fragment in N-protected form and optionally other linear fragments. The
CC products of the invention have osteopathic and hypotensive activity. (II)
CC bind to hPTH receptors and act as agonists or antagonists of hPTH. The
CC method is particularly used to prepare cyclic peptide analogs of
CC parathyroid hormone (PTH) or PTH-related peptides which are useful for
CC treating diseases that respond to treatment with agents that bind to PTH
CC receptors (with or without activation of adenylyl cyclase activity), e.g.
CC hyper- or hypo-calcemia, osteoporosis, osteopenia, hyper- or hypo-
CC parathyroidism, Cushing's syndrome, renal failure and hypertension, also
CC for promoting repair of bone fractures. Separate synthesis of the cyclic
CC fragment allows convergent synthesis of resin-bound (II), with better
CC yields and higher throughput. The difficulties associated with
CC preparation of the bridged fragment are confined to a small peptide which
CC can be purified before reaction with the resin-bound component. AAY50568-
CC Y50614 represent the peptide fragments described in the method of the
CC invention
XX
SQ Sequence 11 AA;

Query Match 73.7%; Score 43.5; DB 2; Length 11;
Best Local Similarity 91.7%; Pred. No. 0.2;
Matches 11; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 AVSEIQLMHNLG 12
||||||| ||||
Db 1 AVSEIQL-HNLG 11

RESULT 10
AAB01862
ID AAB01862 standard; peptide; 9 AA.
XX
AC AAB01862;
XX
DT 11-SEP-2000 (first entry)
XX
DE PTH(1-14)/PTHrP(1-14)-derived peptide, SEQ ID NO:6.
XX
KW Parathyroid hormone peptide; PTH; PTH-related peptide; PTHrP;
KW calcium homeostasis; PTH-1 receptor; PTH-2; vitamin D synthesis;
KW bone synthesis; agonist; osteoporosis; non-parenteral delivery.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200023594-A1.
XX
PD 27-APR-2000.
XX
PF 20-OCT-1999; 99WO-US024481.

```
XX
PR   22-OCT-1998;   98US-0105530P.
XX
PA   (GARD/) GARDELLA T J.
PA   (KRON/) KRONENBERG H M.
PA   (POTT/) POTTS J T.
PA   (JUEP/) JUEPPNER H.
XX
PI   Gardella TJ,  Kronenberg HM,  Potts JT,  Jueppner H;
XX
DR   WPI; 2000-339693/29.
XX
PT   Parathyroid hormone (PTH) peptides, PTH related peptides and the nucleic
PT   acids that encode them, useful for treating osteoporosis.
XX
PS   Disclosure; Page 26; 73pp; English.
XX
CC   The invention relates to a novel parathyroid hormone (PTH) peptide
CC   (AAB01859) and parathyroid hormone-related peptide (PTHrP; AAB01860), and
CC   biologically active derivatives thereof (AAB01857-B01858, AAB01861-
CC   B01869). The peptides of the invention are at least 85% identical to the
CC   generic peptide of the formula: X1-Val-Ser-Glu-X2-Gln-Leu-X3-His-X4-X5-
CC   Gly-Lys-X6 (AAB01857) where: X1 is Ser or Ala; X2 is Ile or Lys; X3 is
CC   Met, Leu or Nle; X4 is Asn or Asp; X5 is Leu or Lys; X6 is His or Ser;
CC   provided that the peptide is not PTHrP(1-14). The peptides of the
CC   invention also encompass fragments of peptides of the invention
CC   consisting of amino acids 1-9, 1-10, 1-11, 1-12 and 1-13, and N- and C-
CC   terminal derivatives. PTH is a major regulator of calcium homeostasis,
CC   and is necessary for the normal function of the gastrointestinal,
CC   skeletal, neurological system, neuromuscular and cardiovascular systems.
CC   It binds to both PTH-1 receptors on osteoblasts and renal tubular cells,
CC   and to the recently identified PTH-2 receptor. PTH has a potent anabolic
CC   effect on the skeleton, and mediates calcium reabsorption, enhances
CC   phosphate clearance and vitamin D synthesis in the kidney. A homologous
CC   calls of protein hormones, the PTH-related proteins (PTHrP) mimic some of
CC   the renal and skeletal actions of PTH, and also bind to the PTH-1
CC   receptor. They do not bind to the PTH-2 receptor. The peptides of the
CC   invention are either agonists of PTH-1 and PTH-2 receptors (AAB01858,
CC   AAB01861-B01866) or are PTH-1/PTH-2 receptor antagonists (AAB01867-
CC   B01869). PTH-1/PTH-2 receptor agonists are useful for the treatment of
CC   conditions characterised by a decrease in bone mass, such as
CC   osteoporosis. PTH-1/PTH-2 receptor antagonists are useful for treating
CC   medical disorders that arise from excessive or altered action of the PTH-
CC   1/PTH-2 receptor. Detectably labelled peptides of the invention are also
CC   useful in the determination of rates of bone formation, bone resorption
CC   and/or bone remodelling in a patient. The peptides of the invention are
CC   "minimised" versions of PTH or PTHrP which are inexpensive to prepare by
CC   conventional synthetic chemistry, and can be delivered to a patient via
CC   non-parenteral routes. Sequences AAB01858 and AAB01861-B01866 represent
CC   PTH-1/PTH-2 receptor agonists
XX
SQ   Sequence 9 AA;

  Query Match             72.9%;  Score 43;  DB 3;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+06;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AVSEIQLMH 9
              |||||||||
Db          1 AVSEIQLMH 9


RESULT 11
AAY96966
ID   AAY96966 standard; peptide; 9 AA.
XX
AC   AAY96966;
XX
DT   31-OCT-2000  (first entry)
XX
DE   Parathyroid hormone N-terminal signaling domain (residues 1-9).
XX
KW   PTH; parathyroid hormone; N-terminal; signaling domain; bone mass;
KW   bone reformation; resorption; remodeling; tether1; osteoporosis.
XX
OS   Homo sapiens.
XX
PN   WO200039278-A2.
XX
PD   06-JUL-2000.
XX
PF   30-DEC-1999;   99WO-US031108.
XX
PR   31-DEC-1998;   98US-0114577P.
XX
PA   (GARD/) GARDELLA T J.
PA   (KRON/) KRONENBERG H M.
PA   (POTT/) POTTS J T.
PA   (JUEP/) JUEPPNER H.
XX
PI   Gardella TJ,  Kronenberg HM,  Potts JT,  Jueppner H;
XX
DR   WPI; 2000-452384/39.
XX
PT   New compound comprising an amino terminal signaling functional domain
PT   linked to a carboxy-terminal binding portion of parathyroid hormone for
PT   treating mammalian conditions characterized by decreases in bone mass.
XX
PS   Claim 4; Page 92; 119pp; English.
XX
CC   Compounds of the structure or formula S-(L)_n-B, R_1-S-(L)_n-R or S-(L)_n
CC   -R, are new. S is an amino terminal signaling functional domain of
CC   parathyroid hormone (PTH); L is a linker molecule present n times (where
CC   n is a positive integer 1-10 (preferably 4)); B is a C-terminal binding
CC   portion of PTH(1-34) or a PTH-related protein (PTH-rP) (1-34); R_1 is the
CC   PTH-1 receptor signal sequence; and R is (a portion of) PTH-1 receptor
CC   sequence. The new compounds are used for treating mammalian conditions
CC   characterized by decreases in bone mass, determining rates of bone
CC   reformation, bone resorption and/or bone remodeling, treating diseases
CC   and disorders associated with decreased tether1 activity, increasing cAMP
CC   in a mammalian cell having PTH-1 receptors, or screening for a peptide or
CC   non-peptide PTH (claimed). The new compound can be administered by
CC   inhalation unlike the large native PTH or PTHrP which avoids the need for
CC   regular injections to treat osteoporosis
XX
SQ   Sequence 9 AA;

  Query Match             72.9%;  Score 43;  DB 3;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+06;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AVSEIQLMH 9
              |||||||||
Db          1 AVSEIQLMH 9


RESULT 12
AAR91645
ID   AAR91645 standard; peptide; 9 AA.
XX
AC   AAR91645;
XX
DT   06-NOV-1996  (first entry)
XX
DE   Human parathyroid hormone antigenic peptide hPTH 1-9.
XX
KW   Human parathyroid hormone; hPTH; antigen; alpha-helix; immunogen;
KW   diagnosis; active hPTH 1-37.
XX
OS   Synthetic.
XX
PN   DE4434551-A1.
XX
PD   04-APR-1996.
XX
PF   28-SEP-1994;   94DE-04434551.
```

```
XX
PR   28-SEP-1994;   94DE-04434551.
XX
PA   (FORS/) FORSSMANN W.
XX
PI   Adermann K,  Forssmann W,  Hock D,  Maegerlein M;
XX
DR   WPI; 1996-180391/19.
XX
PT   New antigenic peptide(s) from human parathyroid hormone - and antibodies
PT   generated using them, able to distinguish between active and inactive
PT   forms of the hormone.
XX
PS   Claim 2; Page 4; 5pp; German.
XX
CC   The present sequence is a specific example of claimed immunogenic
CC   peptides having a sequence from hPTH(1-37) which includes the N- or C-
CC   terminal alpha-helical region and/or the non-structured region of the
CC   hormone. Antibodies and their binding fragments generated by injecting an
CC   animal with the peptides are useful as diagnostic reagents for
CC   determination of biologically active hPTH(1-37)
XX
SQ   Sequence 9 AA;

  Query Match             67.8%;  Score 40;  DB 2;  Length 9;
  Best Local Similarity   88.9%;  Pred. No. 1.4e+06;
  Matches    8;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AVSEIQLMH 9
              :|||||||||
Db          1 SVSEIQLMH 9


RESULT 13
AAB01863
ID   AAB01863 standard; peptide; 9 AA.
XX
AC   AAB01863;
XX
DT   11-SEP-2000  (first entry)
XX
DE   PTH(1-14)/PTHrP(1-14)-derived peptide, SEQ ID NO:7.
XX
KW   Parathyroid hormone peptide; PTH; PTH-related peptide; PTHrP;
KW   calcium homeostasis; PTH-1 receptor; PTH-2; vitamin D synthesis;
KW   bone synthesis; agonist; osteoporosis; non-parenteral delivery.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200023594-A1.
XX
PD   27-APR-2000.
XX
PF   20-OCT-1999;   99WO-US024481.
XX
PR   22-OCT-1998;   98US-0105530P.
XX
PA   (GARD/) GARDELLA T J.
PA   (KRON/) KRONENBERG H M.
PA   (POTT/) POTTS J T.
PA   (JUEP/) JUEPPNER H.
XX
PI   Gardella TJ,  Kronenberg HM,  Potts JT,  Jueppner H;
XX
DR   WPI; 2000-339693/29.
XX
PT   Parathyroid hormone (PTH) peptides, PTH related peptides and the nucleic
PT   acids that encode them, useful for treating osteoporosis.
XX
PS   Disclosure; Page 26; 73pp; English.
XX
CC   The invention relates to a novel parathyroid hormone (PTH) peptide
CC   (AAB01859) and parathyroid hormone-related peptide (PTHrP; AAB01860), and
CC   biologically active derivatives thereof (AAB01857-B01858, AAB01861-
CC   B01869). The peptides of the invention are at least 85% identical to the
CC   generic peptide of the formula: X1-Val-Ser-Glu-X2-Gln-Leu-X3-His-X4-X5-
CC   Gly-Lys-X6 (AAB01857) where: X1 is Ser or Ala; X2 is Ile or Lys; X3 is
CC   Met, Leu or Nle; X4 is Asn or Asp; X5 is Leu or Lys; X6 is His or Ser;
CC   provided that the peptide is not PTHrP(1-14). The peptides of the
CC   invention also encompass fragments of peptides of the invention
CC   consisting of amino acids 1-9, 1-10, 1-11, 1-12 and 1-13, and N- and C-
CC   terminal derivatives. PTH is a major regulator of calcium homeostasis,
CC   and is necessary for the normal function of the gastrointestinal,
CC   skeletal, neurological system, neuromuscular and cardiovascular systems.
CC   It binds to both PTH-1 receptors on osteoblasts and renal tubular cells,
CC   and to the recently identified PTH-2 receptor. PTH has a potent anabolic
CC   effect on the skeleton, and mediates calcium reabsorption, enhances
CC   phosphate clearance and vitamin D synthesis in the kidney. A homologous
CC   calls of protein hormones, the PTH-related proteins (PTHrP) mimic some of
CC   the renal and skeletal actions of PTH, and also bind to the PTH-1
CC   receptor. They do not bind to the PTH-2 receptor. The peptides of the
CC   invention are either agonists of PTH-1 and PTH-2 receptors (AAB01858,
CC   AAB01861-B01866) or are PTH-1/PTH-2 receptor antagonists (AAB01867-
CC   B01869). PTH-1/PTH-2 receptor agonists are useful for the treatment of
CC   conditions characterised by a decrease in bone mass, such as
CC   osteoporosis. PTH-1/PTH-2 receptor antagonists are useful for treating
CC   medical disorders that arise from excessive or altered action of the PTH-
CC   1/PTH-2 receptor. Detectably labelled peptides of the invention are also
CC   useful in the determination of rates of bone formation, bone resorption
CC   and/or bone remodelling in a patient. The peptides of the invention are
CC   "minimised" versions of PTH or PTHrP which are inexpensive to prepare by
CC   conventional synthetic chemistry, and can be delivered to a patient via
CC   non-parenteral routes. Sequences AAB01858 and AAB01861-B01866 represent
CC   PTH-1/PTH-2 receptor agonists
XX
SQ   Sequence 9 AA;

  Query Match             67.8%;  Score 40;  DB 3;  Length 9;
  Best Local Similarity   88.9%;  Pred. No. 1.4e+06;
  Matches    8;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AVSEIQLMH 9
              |||||||:|
Db          1 AVSEIQLLH 9


RESULT 14
AAY96981
ID   AAY96981 standard; peptide; 9 AA.
XX
AC   AAY96981;
XX
DT   31-OCT-2000  (first entry)
XX
DE   Parathyroid hormone N-terminal signaling domain.
XX
KW   PTH; parathyroid hormone; N-terminal; signaling domain; bone mass;
KW   bone reformation; resorption; remodeling; tether1; osteoporosis.
XX
OS   Homo sapiens.
XX
PN   WO200039278-A2.
XX
PD   06-JUL-2000.
XX
PF   30-DEC-1999;   99WO-US031108.
XX
PR   31-DEC-1998;   98US-0114577P.
XX
PA   (GARD/) GARDELLA T J.
PA   (KRON/) KRONENBERG H M.
PA   (POTT/) POTTS J T.
PA   (JUEP/) JUEPPNER H.
XX
PI   Gardella TJ,  Kronenberg HM,  Potts JT,  Jueppner H;
```

XX
DR WPI; 2000-452384/39.
XX
PT New compound comprising an amino terminal signaling functional domain
PT linked to a carboxy-terminal binding portion of parathyroid hormone for
PT treating mammalian conditions characterized by decreases in bone mass.
XX
PS Claim 11; Page 93; 119pp; English.
XX
CC Compounds of the structure or formula S-(L)_n-B, R_1-S-(L)_n-R or S-(L)_n
CC -R, are new. S is an amino terminal signaling functional domain of
CC parathyroid hormone (PTH); L is a linker molecule present n times (where
CC n is a positive integer 1-10 (preferably 4)); B is a C-terminal binding
CC portion of PTH(1-34) or a PTH-related protein (PTH-rP) (1-34); R_1 is the
CC PTH-1 receptor signal sequence; and R is (a portion of) PTH-1 receptor
CC sequence. The new compounds are used for treating mammalian conditions
CC characterized by decreases in bone mass, determining rates of bone
CC reformation, bone resorption and/or bone remodeling, treating diseases
CC and disorders associated with decreased tether1 activity, increasing cAMP
CC in a mammalian cell having PTH-1 receptors, or screening for a peptide or
CC non-peptide PTH (claimed). The new compound can be administered by
CC inhalation unlike the large native PTH or PTHrP which avoids the need for
CC regular injections to treat osteoporosis
XX
SQ Sequence 9 AA;

Query Match 67.8%; Score 40; DB 3; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.4e+06;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AVSEIQLMH 9
:|||||||
Db 1 SVSEIQLMH 9

RESULT 15
AAB86220
ID AAB86220 standard; peptide; 9 AA.
XX
AC AAB86220;
XX
DT 03-SEP-2001 (first entry)
XX
DE Human parathyroid hormone immunogenic peptide SEQ ID 2.
XX
KW Parathyroid hormone; hPTH; immunogenic peptide; human; epitope;
KW diagnosis; calcium-metabolism disorder; osteopathy; antagonist;
KW hypo-parathyroidism; hyper-parathyroidism.
XX
OS Homo sapiens.
XX
PN DE19961350-A1.
XX
PD 21-JUN-2001.
XX
PF 17-DEC-1999; 99DE-01061350.
XX
PR 17-DEC-1999; 99DE-01061350.
XX
PA (IMMU-) IMMUNDIAGNOSTIK AG.
XX
PI Armbruster FP;
XX
DR WPI; 2001-376318/40.
XX
PT Determining the content of physiologically active parathyroid hormone,
PT useful in diagnosis of calcium-metabolism disorders, using two antibodies
PT reactive with different epitopes.
XX
PS Disclosure; Page 3; 10pp; German.
XX
CC This invention describes a novel method for determining (M1) the content
CC of active parathyroid hormone (A) by treating a sample with (i) antibody
CC (Ab1) that recognizes the epitope formed by amino acids (aa) 1-3 of (A),
CC and including the N-terminal residue and (ii) antibody (Ab2) that
CC recognizes an epitope within the receptor-binding site of (A). The number
CC of molecules that react with both antibodies is determined and used to
CC calculate the content of physiologically active (A). The method is used
CC for diagnosis of calcium-metabolism disorders, osteopathy, or hypo- or
CC hyper-parathyroidism. The method (unlike known assays) recognizes that
CC (i) some fragments of (A) shorter than the complete (84 aa) peptide are
CC active and (ii) that apparently intact peptide may be biologically
CC inactive, and also takes into account the fact that some fragments of (A)
CC are antagonistic (these have the receptor-binding site but lack the N-
CC terminus). It thus provides a true measure of the content of
CC physiologically active (A); contrast methods that measure intact peptide
CC and its 1-37 fragment which may produce falsely high values. This
CC sequence represents a peptide fragment used to illustrate the method of
CC the invention
XX
SQ Sequence 9 AA;

Query Match 67.8%; Score 40; DB 4; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.4e+06;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AVSEIQLMH 9
:|||||||
Db 1 SVSEIQLMH 9

Search completed: September 5, 2004, 09:34:30
Job time : 36.5 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: September 5, 2004, 09:37:09 ; Search time 32.5 Seconds
(without alignments)
116.332 Million cell updates/sec

Title: US-09-730-174A-5
Perfect score: 59
Sequence: 1 AVSEIQLMHNLG 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1298764 seqs, 315065143 residues

Total number of hits satisfying chosen parameters: 182187

Minimum DB seq length: 0
Maximum DB seq length: 12

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	59	100.0	12	9	US-09-730-174A-5	Sequence 5, Appli
2	56	94.9	12	9	US-09-730-174A-3	Sequence 3, Appli
3	55	93.2	11	9	US-09-730-174A-1	Sequence 1, Appli
4	55	93.2	12	9	US-09-730-174A-6	Sequence 6, Appli
5	52	88.1	12	9	US-09-730-174A-4	Sequence 4, Appli
6	51	86.4	11	9	US-09-730-174A-2	Sequence 2, Appli
7	46	78.0	10	14	US-10-168-185-1	Sequence 1, Appli
8	45	76.3	9	14	US-10-168-185-7	Sequence 7, Appli
9	43	72.9	9	14	US-10-192-673-6	Sequence 6, Appli
10	41	69.5	8	14	US-10-168-185-8	Sequence 8, Appli
11	40	67.8	9	14	US-10-192-673-7	Sequence 7, Appli
12	40	67.8	9	14	US-10-168-185-2	Sequence 2, Appli
13	33	55.9	9	14	US-10-192-673-8	Sequence 8, Appli
14	32	54.2	8	14	US-10-168-185-3	Sequence 3, Appli
15	30	50.8	9	14	US-10-192-673-10	Sequence 10, Appl
16	28	47.5	12	14	US-10-319-130-16	Sequence 16, Appl
17	27	45.8	7	14	US-10-168-185-4	Sequence 4, Appli
18	27	45.8	10	16	US-10-432-234A-75	Sequence 75, Appl
19	27	45.8	10	16	US-10-432-234A-76	Sequence 76, Appl
20	27	45.8	10	16	US-10-432-234A-77	Sequence 77, Appl
21	27	45.8	11	16	US-10-391-364-93	Sequence 93, Appl
22	26	44.1	10	14	US-10-033-741-61	Sequence 61, Appl
23	25	42.4	9	9	US-09-746-945-6	Sequence 6, Appli
24	25	42.4	10	16	US-10-432-234A-74	Sequence 74, Appl
25	25	42.4	11	12	US-09-747-287-185	Sequence 185, App
26	25	42.4	11	12	US-09-874-350A-151	Sequence 151, App
27	24	40.7	10	9	US-09-826-290-27	Sequence 27, Appl
28	24	40.7	10	16	US-10-264-309-369	Sequence 369, App
29	24	40.7	11	12	US-10-609-217-41	Sequence 41, Appl
30	24	40.7	11	12	US-10-632-388-41	Sequence 41, Appl
31	24	40.7	11	12	US-10-651-723-41	Sequence 41, Appl
32	24	40.7	11	12	US-10-645-761-41	Sequence 41, Appl
33	24	40.7	11	16	US-10-666-696-41	Sequence 41, Appl
34	24	40.7	11	16	US-10-653-048-41	Sequence 41, Appl
35	24	40.7	12	14	US-10-286-457-294	Sequence 294, App
36	23	39.0	6	14	US-10-168-185-5	Sequence 5, Appli
37	23	39.0	7	14	US-10-286-457-469	Sequence 469, App
38	23	39.0	7	15	US-10-368-280-12	Sequence 12, Appl
39	23	39.0	7	15	US-10-374-035-12	Sequence 12, Appl
40	23	39.0	9	9	US-09-894-018-332	Sequence 332, App
41	23	39.0	9	10	US-09-821-734-4	Sequence 4, Appli
42	23	39.0	9	10	US-09-854-248-11	Sequence 11, Appl
43	23	39.0	9	12	US-10-253-286-288	Sequence 288, App
44	23	39.0	9	14	US-10-094-699-50	Sequence 50, Appl
45	23	39.0	9	15	US-10-117-937-249	Sequence 249, App

ALIGNMENTS

RESULT 1
US-09-730-174A-5
; Sequence 5, Application US/09730174A
; Patent No. US20020110871A1
; GENERAL INFORMATION:
; APPLICANT: Zahradnik, R.J.
; TITLE OF INVENTION: Antibodies and Peptide Antigens for Producing Antibodies having
; TITLE OF INVENTION: Selective Binding Specificity to Bioactive Intact Parathyroid H
; FILE REFERENCE: IMUNE-001A
; CURRENT APPLICATION NUMBER: US/09/730,174A
; CURRENT FILING DATE: 2000-12-05
; NUMBER OF SEQ ID NOS: 12
; SEQ ID NO 5
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Induces Formation of Antibodies and Isolates said Antibodies
US-09-730-174A-5

Query Match 100.0%; Score 59; DB 9; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.00072;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 AVSEIQLMHNLG 12
              ||||||||||||
Db          1 AVSEIQLMHNLG 12
```

RESULT 2
US-09-730-174A-3
; Sequence 3, Application US/09730174A
; Patent No. US20020110871A1
; GENERAL INFORMATION:
; APPLICANT: Zahradnik, R.J.
; TITLE OF INVENTION: Antibodies and Peptide Antigens for Producing Antibodies having
; TITLE OF INVENTION: Selective Binding Specificity to Bioactive Intact Parathyroid Hc
; FILE REFERENCE: IMUNE-001A

```
;  CURRENT APPLICATION NUMBER: US/09/730,174A
;  CURRENT FILING DATE:  2000-12-05
;  NUMBER OF SEQ ID NOS: 12
; SEQ ID NO 3
;   LENGTH: 12
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Induces Formation of Antibodies and Isolates said Antibodies
US-09-730-174A-3

  Query Match             94.9%;  Score 56;  DB 9;  Length 12;
  Best Local Similarity   91.7%;  Pred. No. 0.0025;
  Matches   11;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AVSEIQLMHNLG 12
              :||||||||||||
Db          1 SVSEIQLMHNLG 12


RESULT 3
US-09-730-174A-1
; Sequence 1, Application US/09730174A
; Patent No. US20020110871A1
; GENERAL INFORMATION:
;  APPLICANT: Zahradnik, R.J.
;  TITLE OF INVENTION: Antibodies and Peptide Antigens for Producing Antibodies having a
;  TITLE OF INVENTION:  Selective Binding Specificity to Bioactive Intact Parathyroid Ho
;  FILE REFERENCE: IMUNE-001A
;  CURRENT APPLICATION NUMBER: US/09/730,174A
;  CURRENT FILING DATE:  2000-12-05
;  NUMBER OF SEQ ID NOS: 12
; SEQ ID NO 1
;   LENGTH: 11
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Induces Formation of Antibodies and Isolates said Antibodies
US-09-730-174A-1

  Query Match             93.2%;  Score 55;  DB 9;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 0.0034;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 VSEIQLMHNLG 12
              ||||||||||||
Db          1 VSEIQLMHNLG 11


RESULT 4
US-09-730-174A-6
; Sequence 6, Application US/09730174A
; Patent No. US20020110871A1
; GENERAL INFORMATION:
;  APPLICANT: Zahradnik, R.J.
;  TITLE OF INVENTION: Antibodies and Peptide Antigens for Producing Antibodies having a
;  TITLE OF INVENTION:  Selective Binding Specificity to Bioactive Intact Parathyroid Ho
;  FILE REFERENCE: IMUNE-001A
;  CURRENT APPLICATION NUMBER: US/09/730,174A
;  CURRENT FILING DATE:  2000-12-05
;  NUMBER OF SEQ ID NOS: 12
; SEQ ID NO 6
;   LENGTH: 12
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Induces Formation of Antibodies and Isolates said Antibodies
US-09-730-174A-6

  Query Match             93.2%;  Score 55;  DB 9;  Length 12;
  Best Local Similarity   91.7%;  Pred. No. 0.0037;
  Matches   11;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 AVSEIQLMHNLG 12
              ||||||.|||||
Db          1 AVSEIQFMHNLG 12


RESULT 5
US-09-730-174A-4
; Sequence 4, Application US/09730174A
; Patent No. US20020110871A1
; GENERAL INFORMATION:
;  APPLICANT: Zahradnik, R.J.
;  TITLE OF INVENTION: Antibodies and Peptide Antigens for Producing Antibodies having a
;  TITLE OF INVENTION:  Selective Binding Specificity to Bioactive Intact Parathyroid Ho
;  FILE REFERENCE: IMUNE-001A
;  CURRENT APPLICATION NUMBER: US/09/730,174A
;  CURRENT FILING DATE:  2000-12-05
;  NUMBER OF SEQ ID NOS: 12
; SEQ ID NO 4
;   LENGTH: 12
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Induces Formation of Antibodies and Isolates said Antibodies
US-09-730-174A-4

  Query Match             88.1%;  Score 52;  DB 9;  Length 12;
  Best Local Similarity   83.3%;  Pred. No. 0.013;
  Matches   10;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 AVSEIQLMHNLG 12
              :|||||.|||||
Db          1 SVSEIQFMHNLG 12


RESULT 6
US-09-730-174A-2
; Sequence 2, Application US/09730174A
; Patent No. US20020110871A1
; GENERAL INFORMATION:
;  APPLICANT: Zahradnik, R.J.
;  TITLE OF INVENTION: Antibodies and Peptide Antigens for Producing Antibodies having a
;  TITLE OF INVENTION:  Selective Binding Specificity to Bioactive Intact Parathyroid Ho
;  FILE REFERENCE: IMUNE-001A
;  CURRENT APPLICATION NUMBER: US/09/730,174A
;  CURRENT FILING DATE:  2000-12-05
;  NUMBER OF SEQ ID NOS: 12
; SEQ ID NO 2
;   LENGTH: 11
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Induces Formation of Antibodies and Isolates said Antibodies
US-09-730-174A-2

  Query Match             86.4%;  Score 51;  DB 9;  Length 11;
  Best Local Similarity   90.9%;  Pred. No. 0.018;
  Matches   10;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 VSEIQLMHNLG 12
              |||||.|||||
Db          1 VSEIQFMHNLG 11


RESULT 7
US-10-168-185-1
; Sequence 1, Application US/10168185
; Publication No. US20030175802A1
; GENERAL INFORMATION:
;  APPLICANT: Armbruster, Franz Paul
;  APPLICANT:  Missbichler, Albert
;  APPLICANT:  Schmidt-Gayk, Heinrich
;  APPLICANT:  Roth, Heinz-Jurgen
;  TITLE OF INVENTION: Method for Determining Parathormone
```

```
;  TITLE OF INVENTION:  Activity in a Human Sample
;  FILE REFERENCE: HLZ-004US
;  CURRENT APPLICATION NUMBER: US/10/168,185
;  CURRENT FILING DATE:  2002-06-17
;  PRIOR APPLICATION NUMBER: PCT/EP00/12911
;  PRIOR FILING DATE: 2000-12-18
;  PRIOR APPLICATION NUMBER: DE 19961350
;  PRIOR FILING DATE: 1999-12-17
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 10
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-168-185-1

  Query Match             78.0%;  Score 46;  DB 14;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 0.13;
  Matches    9;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AVSEIQLMHN 10
              :|||||||||
Db          1 SVSEIQLMHN 10


RESULT 8
US-10-168-185-7
; Sequence 7, Application US/10168185
; Publication No. US20030175802A1
; GENERAL INFORMATION:
;  APPLICANT: Armbruster, Franz Paul
;  APPLICANT:  Missbichler, Albert
;  APPLICANT:  Schmidt-Gayk, Heinrich
;  APPLICANT:  Roth, Heinz-Jurgen
;  TITLE OF INVENTION: Method for Determining Parathormone
;  TITLE OF INVENTION:  Activity in a Human Sample
;  FILE REFERENCE: HLZ-004US
;  CURRENT APPLICATION NUMBER: US/10/168,185
;  CURRENT FILING DATE:  2002-06-17
;  PRIOR APPLICATION NUMBER: PCT/EP00/12911
;  PRIOR FILING DATE: 2000-12-18
;  PRIOR APPLICATION NUMBER: DE 19961350
;  PRIOR FILING DATE: 1999-12-17
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-168-185-7

  Query Match             76.3%;  Score 45;  DB 14;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+06;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 VSEIQLMHN 10
              |||||||||
Db          1 VSEIQLMHN 9


RESULT 9
US-10-192-673-6
; Sequence 6, Application US/10192673
; Publication No. US20030166838A1
; GENERAL INFORMATION:
;  APPLICANT: Gardella, Thomas J.
;  APPLICANT:  Kronenberg, Henry
;  APPLICANT:  Potts, John T.
;  APPLICANT:  Juppner, Harald
;  TITLE OF INVENTION: Bioactive Peptides and Peptide Derivatives of
;  TITLE OF INVENTION:  Parathyroid Hormone (PTH) and Parathyroid
;  TITLE OF INVENTION:  Hormone-Related Peptide (PTHrP)
;  FILE REFERENCE: 0609.4570002
;  CURRENT APPLICATION NUMBER: US/10/192,673
;  CURRENT FILING DATE:  2002-07-11
;  PRIOR APPLICATION NUMBER: U.S. 09/421,379
;  PRIOR FILING DATE: 1999-10-20
;  PRIOR APPLICATION NUMBER: U.S. 60/105,530
;  PRIOR FILING DATE: 1998-10-22
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: synthetic
;   OTHER INFORMATION: peptide
US-10-192-673-6

  Query Match             72.9%;  Score 43;  DB 14;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+06;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AVSEIQLMH 9
              |||||||||
Db          1 AVSEIQLMH 9


RESULT 10
US-10-168-185-8
; Sequence 8, Application US/10168185
; Publication No. US20030175802A1
; GENERAL INFORMATION:
;  APPLICANT: Armbruster, Franz Paul
;  APPLICANT:  Missbichler, Albert
;  APPLICANT:  Schmidt-Gayk, Heinrich
;  APPLICANT:  Roth, Heinz-Jurgen
;  TITLE OF INVENTION: Method for Determining Parathormone
;  TITLE OF INVENTION:  Activity in a Human Sample
;  FILE REFERENCE: HLZ-004US
;  CURRENT APPLICATION NUMBER: US/10/168,185
;  CURRENT FILING DATE:  2002-06-17
;  PRIOR APPLICATION NUMBER: PCT/EP00/12911
;  PRIOR FILING DATE: 2000-12-18
;  PRIOR APPLICATION NUMBER: DE 19961350
;  PRIOR FILING DATE: 1999-12-17
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
;   LENGTH: 8
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-168-185-8

  Query Match             69.5%;  Score 41;  DB 14;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+06;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 SEIQLMHN 10
              ||||||||
Db          1 SEIQLMHN 8


RESULT 11
US-10-192-673-7
; Sequence 7, Application US/10192673
; Publication No. US20030166838A1
; GENERAL INFORMATION:
;  APPLICANT: Gardella, Thomas J.
;  APPLICANT:  Kronenberg, Henry
;  APPLICANT:  Potts, John T.
;  APPLICANT:  Juppner, Harald
;  TITLE OF INVENTION: Bioactive Peptides and Peptide Derivatives of
;  TITLE OF INVENTION:  Parathyroid Hormone (PTH) and Parathyroid
;  TITLE OF INVENTION:  Hormone-Related Peptide (PTHrP)
```

```
;  FILE REFERENCE: 0609.4570002
;  CURRENT APPLICATION NUMBER: US/10/192,673
;  CURRENT FILING DATE:  2002-07-11
;  PRIOR APPLICATION NUMBER: U.S. 09/421,379
;  PRIOR FILING DATE: 1999-10-20
;  PRIOR APPLICATION NUMBER: U.S. 60/105,530
;  PRIOR FILING DATE: 1998-10-22
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: synthetic
;   OTHER INFORMATION: peptide
US-10-192-673-7

  Query Match             67.8%;  Score 40;  DB 14;  Length 9;
  Best Local Similarity   88.9%;  Pred. No. 1.2e+06;
  Matches    8;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AVSEIQLMH 9
              |||||||:|
Db          1 AVSEIQLLH 9


RESULT 12
US-10-168-185-2
; Sequence 2, Application US/10168185
; Publication No. US20030175802A1
; GENERAL INFORMATION:
;  APPLICANT: Armbruster, Franz Paul
;  APPLICANT:  Missbichler, Albert
;  APPLICANT:  Schmidt-Gayk, Heinrich
;  APPLICANT:  Roth, Heinz-Jurgen
;  TITLE OF INVENTION: Method for Determining Parathormone
;  TITLE OF INVENTION:  Activity in a Human Sample
;  FILE REFERENCE: HLZ-004US
;  CURRENT APPLICATION NUMBER: US/10/168,185
;  CURRENT FILING DATE:  2002-06-17
;  PRIOR APPLICATION NUMBER: PCT/EP00/12911
;  PRIOR FILING DATE: 2000-12-18
;  PRIOR APPLICATION NUMBER: DE 19961350
;  PRIOR FILING DATE: 1999-12-17
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-168-185-2

  Query Match             67.8%;  Score 40;  DB 14;  Length 9;
  Best Local Similarity   88.9%;  Pred. No. 1.2e+06;
  Matches    8;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AVSEIQLMH 9
              :|||||||:
Db          1 SVSEIQLMH 9


RESULT 13
US-10-192-673-8
; Sequence 8, Application US/10192673
; Publication No. US20030166838A1
; GENERAL INFORMATION:
;  APPLICANT: Gardella, Thomas J.
;  APPLICANT:  Kronenberg, Henry
;  APPLICANT:  Potts, John T.
;  APPLICANT:  Juppner, Harald
;  TITLE OF INVENTION: Bioactive Peptides and Peptide Derivatives of
;  TITLE OF INVENTION:  Parathyroid Hormone (PTH) and Parathyroid
;  TITLE OF INVENTION:  Hormone-Related Peptide (PTHrP)
;  FILE REFERENCE: 0609.4570002
;  CURRENT APPLICATION NUMBER: US/10/192,673
;  CURRENT FILING DATE:  2002-07-11
;  PRIOR APPLICATION NUMBER: U.S. 09/421,379
;  PRIOR FILING DATE: 1999-10-20
;  PRIOR APPLICATION NUMBER: U.S. 60/105,530
;  PRIOR FILING DATE: 1998-10-22
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: synthetic
;   OTHER INFORMATION: peptide
US-10-192-673-8

  Query Match             55.9%;  Score 33;  DB 14;  Length 9;
  Best Local Similarity   77.8%;  Pred. No. 1.2e+06;
  Matches    7;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 AVSEIQLMH 9
              ||||  ||:|
Db          1 AVSEHQLLH 9


RESULT 14
US-10-168-185-3
; Sequence 3, Application US/10168185
; Publication No. US20030175802A1
; GENERAL INFORMATION:
;  APPLICANT: Armbruster, Franz Paul
;  APPLICANT:  Missbichler, Albert
;  APPLICANT:  Schmidt-Gayk, Heinrich
;  APPLICANT:  Roth, Heinz-Jurgen
;  TITLE OF INVENTION: Method for Determining Parathormone
;  TITLE OF INVENTION:  Activity in a Human Sample
;  FILE REFERENCE: HLZ-004US
;  CURRENT APPLICATION NUMBER: US/10/168,185
;  CURRENT FILING DATE:  2002-06-17
;  PRIOR APPLICATION NUMBER: PCT/EP00/12911
;  PRIOR FILING DATE: 2000-12-18
;  PRIOR APPLICATION NUMBER: DE 19961350
;  PRIOR FILING DATE: 1999-12-17
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;   LENGTH: 8
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-168-185-3

  Query Match             54.2%;  Score 32;  DB 14;  Length 8;
  Best Local Similarity   87.5%;  Pred. No. 1.2e+06;
  Matches    7;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AVSEIQLM 8
              :|||||||
Db          1 SVSEIQLM 8


RESULT 15
US-10-192-673-10
; Sequence 10, Application US/10192673
; Publication No. US20030166838A1
; GENERAL INFORMATION:
;  APPLICANT: Gardella, Thomas J.
;  APPLICANT:  Kronenberg, Henry
;  APPLICANT:  Potts, John T.
;  APPLICANT:  Juppner, Harald
;  TITLE OF INVENTION: Bioactive Peptides and Peptide Derivatives of
```

```
;  TITLE OF INVENTION:  Parathyroid Hormone (PTH) and Parathyroid
;  TITLE OF INVENTION:  Hormone-Related Peptide (PTHrP)
;  FILE REFERENCE: 0609.4570002
;  CURRENT APPLICATION NUMBER: US/10/192,673
;  CURRENT FILING DATE:  2002-07-11
;  PRIOR APPLICATION NUMBER: U.S. 09/421,379
;  PRIOR FILING DATE: 1999-10-20
;  PRIOR APPLICATION NUMBER: U.S. 60/105,530
;  PRIOR FILING DATE: 1998-10-22
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: synthetic
;   OTHER INFORMATION: peptide
US-10-192-673-10

  Query Match           50.8%;  Score 30;  DB 14;  Length 9;
  Best Local Similarity  66.7%;  Pred. No. 1.2e+06;
  Matches    6;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 AVSEIQLMH 9
              :|||| ||:|
Db          1 SVSEHQLLH 9


Search completed: September  5, 2004, 09:49:38
Job time : 32.5 secs
```

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: September 5, 2004, 09:32:03 ; Search time 11 Seconds
(without alignments)
56.319 Million cell updates/sec

Title: US-09-730-174A-5
Perfect score: 59
Sequence: 1 AVSEIQLMHNLG 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 121490

Minimum DB seq length: 0
Maximum DB seq length: 12

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	53	89.8	12	4	US-09-442-989-31	Sequence 31, Appl
2	46	78.0	10	3	US-08-817-547A-1	Sequence 1, Appli
3	43	72.9	9	4	US-09-421-379-6	Sequence 6, Appli
4	40	67.8	9	3	US-08-817-547A-2	Sequence 2, Appli
5	40	67.8	9	4	US-09-421-379-7	Sequence 7, Appli
6	35	59.3	11	6	5460978-3	Patent No. 5460978
7	33	55.9	9	4	US-09-421-379-8	Sequence 8, Appli
8	32	54.2	8	3	US-08-817-547A-3	Sequence 3, Appli
9	30	50.8	9	4	US-09-421-379-10	Sequence 10, Appl
10	27	45.8	7	3	US-08-817-547A-4	Sequence 4, Appli
11	25	42.4	10	2	US-08-428-257A-14	Sequence 14, Appl
12	25	42.4	11	3	US-08-802-981-124	Sequence 124, App
13	24	40.7	5	2	US-08-177-109A-56	Sequence 56, Appl
14	24	40.7	5	2	US-08-687-706-56	Sequence 56, Appl
15	24	40.7	5	3	US-08-817-547A-17	Sequence 17, Appl
16	24	40.7	6	3	US-08-817-547A-16	Sequence 16, Appl
17	24	40.7	7	3	US-08-817-547A-15	Sequence 15, Appl
18	24	40.7	8	2	US-08-748-021-64	Sequence 64, Appl
19	24	40.7	8	3	US-08-817-547A-14	Sequence 14, Appl
20	24	40.7	8	3	US-08-974-297-64	Sequence 64, Appl
21	24	40.7	9	3	US-08-817-547A-13	Sequence 13, Appl
22	24	40.7	10	3	US-08-817-547A-7	Sequence 7, Appli
23	24	40.7	11	2	US-08-726-464B-13	Sequence 13, Appl
24	24	40.7	11	4	US-09-428-082B-41	Sequence 41, Appl
25	23	39.0	6	3	US-08-817-547A-5	Sequence 5, Appli
26	23	39.0	7	4	US-09-336-093-12	Sequence 12, Appl
27	23	39.0	7	4	US-09-557-465D-12	Sequence 12, Appl
28	23	39.0	10	3	US-08-396-385-6	Sequence 6, Appli
29	23	39.0	10	4	US-09-287-221-6	Sequence 6, Appli
30	23	39.0	12	2	US-08-140-137A-42	Sequence 42, Appl
31	23	39.0	12	4	US-08-474-349A-271	Sequence 271, App
32	22	37.3	8	3	US-08-160-604-74	Sequence 74, Appl
33	22	37.3	8	3	US-08-160-604-75	Sequence 75, Appl
34	22	37.3	8	4	US-09-296-089-10	Sequence 10, Appl
35	22	37.3	8	4	US-09-551-976-10	Sequence 10, Appl
36	22	37.3	9	4	US-09-492-543-177	Sequence 177, App
37	22	37.3	11	3	US-08-652-877-71	Sequence 71, Appl
38	22	37.3	11	3	US-08-160-604-73	Sequence 73, Appl
39	22	37.3	11	3	US-08-476-515A-71	Sequence 71, Appl
40	22	37.3	11	4	US-09-296-089-27	Sequence 27, Appl
41	22	37.3	11	4	US-08-475-955-56	Sequence 56, Appl
42	22	37.3	11	4	US-09-551-976-27	Sequence 27, Appl
43	22	37.3	12	4	US-09-690-454-89	Sequence 89, Appl
44	22	37.3	12	4	US-09-591-694-41	Sequence 41, Appl
45	21	35.6	6	2	US-08-621-803-184	Sequence 184, App

ALIGNMENTS

```
RESULT 1
US-09-442-989-31
; Sequence 31, Application US/09442989
; Patent No. 6569993
; GENERAL INFORMATION:
;  APPLICANT: Sledeski, Adam W.
;  APPLICANT: Mencel, James J.
;  TITLE OF INVENTION: PROCESS FOR THE PREPARATION OF RESIN-BOUND CYCLIC
;  TITLE OF INVENTION: PEPTIDES
;  FILE REFERENCE: A3113B-US
;  CURRENT APPLICATION NUMBER: US/09/442,989
;  CURRENT FILING DATE: 1999-11-18
;  EARLIER APPLICATION NUMBER: 60/081,897
;  EARLIER FILING DATE: 1998-04-15
;  NUMBER OF SEQ ID NOS: 46
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 31
;   LENGTH: 12
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: PEPTIDE
;   LOCATION: (1)
;   OTHER INFORMATION: FMOC-Ala
;   FEATURE:
;   NAME/KEY: PEPTIDE
;   LOCATION: (3)
;   OTHER INFORMATION: Ser(OtBu)
;   FEATURE:
;   NAME/KEY: PEPTIDE
;   LOCATION: (4)
;   OTHER INFORMATION: Glu(OtBu)
;   FEATURE:
;   NAME/KEY: PEPTIDE
;   LOCATION: (6)
;   OTHER INFORMATION: Gln(Trt)
;   FEATURE:
;   NAME/KEY: PEPTIDE
;   LOCATION: (9)
;   OTHER INFORMATION: His(Trt)
;   FEATURE:
;   NAME/KEY: PEPTIDE
;   LOCATION: (10)
;   OTHER INFORMATION: Asn(Trt)
;   FEATURE:
;   NAME/KEY: MOD_RES
;   LOCATION: (8)
;   OTHER INFORMATION: Nle
US-09-442-989-31
```

```
  Query Match             89.8%;  Score 53;  DB 4;  Length 12;
  Best Local Similarity   91.7%;  Pred. No. 0.0012;
  Matches   11;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 AVSEIQLMHNLG 12
              ||||||| ||||
Db          1 AVSEIQLXHNLG 12


RESULT 2
US-08-817-547A-1
; Sequence 1, Application US/08817547A
; Patent No. 6030790
;  GENERAL INFORMATION:
;    APPLICANT:  Adermann, Knut
;    APPLICANT:  Hock, Dieter
;    APPLICANT:  Magerlein, Markus
;    TITLE OF INVENTION:  Peptides from the hPTH Sequence
;    NUMBER OF SEQUENCES:  36
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Jones & Askew, LLP
;      STREET:  191 Peachtree Street, 37th Floor
;      CITY:  Atlanta
;      STATE:  Georgia
;      COUNTRY:  USA
;      ZIP:  30303
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/817,547A
;      FILING DATE:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/EP95/03757
;      FILING DATE:  29 SEPT 1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  FROST, ROGER T.
;      REGISTRATION NUMBER:  22,176
;      REFERENCE/DOCKET NUMBER:  07826-0007
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  404-818-3700
;      TELEFAX:  404-818-3799
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  unknown
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  peptide
;    HYPOTHETICAL:  no
;    ANTI-SENSE:  no
US-08-817-547A-1

  Query Match             78.0%;  Score 46;  DB 3;  Length 10;
  Best Local Similarity   90.0%;  Pred. No. 0.019;
  Matches    9;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AVSEIQLMHN 10
              :|||||||||
Db          1 SVSEIQLMHN 10


RESULT 3
US-09-421-379-6
; Sequence 6, Application US/09421379
; Patent No. 6495662
; GENERAL INFORMATION:
;  APPLICANT: Gardella, Thomas J.
;  APPLICANT: Kronenberg, Henry
;  APPLICANT: Potts, John T.
;  APPLICANT: Juppner, Harald
;  TITLE OF INVENTION: Bioactive Peptides and Peptide Derivatives of
;  TITLE OF INVENTION: Parathyroid Hormone (PTH) and Parathyroid
;  TITLE OF INVENTION: Hormone-Related Peptide (PTHrP)
;  FILE REFERENCE: 0609.4570001
;  CURRENT APPLICATION NUMBER: US/09/421,379
;  CURRENT FILING DATE: 1999-10-20
;  EARLIER APPLICATION NUMBER: U.S. 60/105,530
;  EARLIER FILING DATE: 1998-10-22
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: synthetic
;   OTHER INFORMATION: peptide
US-09-421-379-6

  Query Match             72.9%;  Score 43;  DB 4;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 3e+05;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AVSEIQLMH 9
              |||||||||
Db          1 AVSEIQLMH 9


RESULT 4
US-08-817-547A-2
; Sequence 2, Application US/08817547A
; Patent No. 6030790
;  GENERAL INFORMATION:
;    APPLICANT:  Adermann, Knut
;    APPLICANT:  Hock, Dieter
;    APPLICANT:  Magerlein, Markus
;    TITLE OF INVENTION:  Peptides from the hPTH Sequence
;    NUMBER OF SEQUENCES:  36
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Jones & Askew, LLP
;      STREET:  191 Peachtree Street, 37th Floor
;      CITY:  Atlanta
;      STATE:  Georgia
;      COUNTRY:  USA
;      ZIP:  30303
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/817,547A
;      FILING DATE:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/EP95/03757
;      FILING DATE:  29 SEPT 1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  FROST, ROGER T.
;      REGISTRATION NUMBER:  22,176
;      REFERENCE/DOCKET NUMBER:  07826-0007
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  404-818-3700
;      TELEFAX:  404-818-3799
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  9 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  unknown
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  peptide
;    HYPOTHETICAL:  no
;    ANTI-SENSE:  no
US-08-817-547A-2
```

```
  Query Match             67.8%;  Score 40;  DB 3;  Length 9;
  Best Local Similarity   88.9%;  Pred. No. 3e+05;
  Matches    8;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AVSEIQLMH 9
              :|||||||||
Db          1 SVSEIQLMH 9


RESULT 5
US-09-421-379-7
; Sequence 7, Application US/09421379
; Patent No. 6495662
; GENERAL INFORMATION:
;  APPLICANT: Gardella, Thomas J.
;  APPLICANT: Kronenberg, Henry
;  APPLICANT: Potts, John T.
;  APPLICANT: Juppner, Harald
;  TITLE OF INVENTION: Bioactive Peptides and Peptide Derivatives of
;  TITLE OF INVENTION: Parathyroid Hormone (PTH) and Parathyroid
;  TITLE OF INVENTION: Hormone-Related Peptide (PTHrP)
;  FILE REFERENCE: 0609.4570001
;  CURRENT APPLICATION NUMBER: US/09/421,379
;  CURRENT FILING DATE: 1999-10-20
;  EARLIER APPLICATION NUMBER: U.S. 60/105,530
;  EARLIER FILING DATE: 1998-10-22
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: synthetic
;   OTHER INFORMATION: peptide
US-09-421-379-7

  Query Match             67.8%;  Score 40;  DB 4;  Length 9;
  Best Local Similarity   88.9%;  Pred. No. 3e+05;
  Matches    8;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AVSEIQLMH 9
              |||||||:|
Db          1 AVSEIQLLH 9


RESULT 6
5460978-3
;Patent No. 5460978
;    APPLICANT: MARTIN, THOMAS J.;MOSELEY, JANE M.;KEMP,
;BRUCE E.;WETTENHALL, RICHARD E.H.
;    TITLE OF INVENTION: PROTEIN ACTIVE IN HUMORAL
;HYPERCALCEMIA OF MALIGNANCY-PTHRP
;    NUMBER OF SEQUENCES: 4
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/715,280
;      FILING DATE: 14-JUN-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER: 199,235
;      FILING DATE: 09-MAY-1988
;      APPLICATION NUMBER:
;      FILING DATE:
;SEQ ID NO:3:
;      LENGTH: 11
5460978-3

  Query Match             59.3%;  Score 35;  DB 6;  Length 11;
  Best Local Similarity   80.0%;  Pred. No. 2.2;
  Matches    8;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 AVSEIQLMHN 10
              |||| || ||
Db          1 AVSEHQLEHN 10


RESULT 7
US-09-421-379-8
; Sequence 8, Application US/09421379
; Patent No. 6495662
; GENERAL INFORMATION:
;  APPLICANT: Gardella, Thomas J.
;  APPLICANT: Kronenberg, Henry
;  APPLICANT: Potts, John T.
;  APPLICANT: Juppner, Harald
;  TITLE OF INVENTION: Bioactive Peptides and Peptide Derivatives of
;  TITLE OF INVENTION: Parathyroid Hormone (PTH) and Parathyroid
;  TITLE OF INVENTION: Hormone-Related Peptide (PTHrP)
;  FILE REFERENCE: 0609.4570001
;  CURRENT APPLICATION NUMBER: US/09/421,379
;  CURRENT FILING DATE: 1999-10-20
;  EARLIER APPLICATION NUMBER: U.S. 60/105,530
;  EARLIER FILING DATE: 1998-10-22
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: synthetic
;   OTHER INFORMATION: peptide
US-09-421-379-8

  Query Match             55.9%;  Score 33;  DB 4;  Length 9;
  Best Local Similarity   77.8%;  Pred. No. 3e+05;
  Matches    7;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 AVSEIQLMH 9
              |||| ||:|
Db          1 AVSEHQLLH 9


RESULT 8
US-08-817-547A-3
; Sequence 3, Application US/08817547A
; Patent No. 6030790
;  GENERAL INFORMATION:
;    APPLICANT:  Adermann, Knut
;    APPLICANT:  Hock, Dieter
;    APPLICANT:  Magerlein, Markus
;    TITLE OF INVENTION:  Peptides from the hPTH Sequence
;    NUMBER OF SEQUENCES:  36
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Jones & Askew, LLP
;      STREET:  191 Peachtree Street, 37th Floor
;      CITY:  Atlanta
;      STATE:  Georgia
;      COUNTRY:  USA
;      ZIP:  30303
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/817,547A
;      FILING DATE:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/EP95/03757
;      FILING DATE:  29 SEPT 1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  FROST, ROGER T.
;      REGISTRATION NUMBER:  22,176
;      REFERENCE/DOCKET NUMBER:  07826-0007
;    TELECOMMUNICATION INFORMATION:
```

```
;       TELEPHONE:  404-818-3700
;       TELEFAX:  404-818-3799
;   INFORMATION FOR SEQ ID NO:  3:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  8 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:  unknown
;       TOPOLOGY:  unknown
;     MOLECULE TYPE:  peptide
;     HYPOTHETICAL:  no
;     ANTI-SENSE:  no
US-08-817-547A-3

  Query Match             54.2%;  Score 32;  DB 3;  Length 8;
  Best Local Similarity   87.5%;  Pred. No. 3e+05;
  Matches    7;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AVSEIQLM 8
              :|||||||
Db          1 SVSEIQLM 8


RESULT 9
US-09-421-379-10
; Sequence 10, Application US/09421379
; Patent No. 6495662
; GENERAL INFORMATION:
;  APPLICANT: Gardella, Thomas J.
;  APPLICANT: Kronenberg, Henry
;  APPLICANT: Potts, John T.
;  APPLICANT: Juppner, Harald
;  TITLE OF INVENTION: Bioactive Peptides and Peptide Derivatives of
;  TITLE OF INVENTION: Parathyroid Hormone (PTH) and Parathyroid
;  TITLE OF INVENTION: Hormone-Related Peptide (PTHrP)
;  FILE REFERENCE: 0609.4570001
;  CURRENT APPLICATION NUMBER: US/09/421,379
;  CURRENT FILING DATE: 1999-10-20
;  EARLIER APPLICATION NUMBER: U.S. 60/105,530
;  EARLIER FILING DATE: 1998-10-22
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: synthetic
;   OTHER INFORMATION: peptide
US-09-421-379-10

  Query Match             50.8%;  Score 30;  DB 4;  Length 9;
  Best Local Similarity   66.7%;  Pred. No. 3e+05;
  Matches    6;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 AVSEIQLMH 9
              :||| ||:|
Db          1 SVSEHQLLH 9


RESULT 10
US-08-817-547A-4
; Sequence 4, Application US/08817547A
; Patent No. 6030790
;  GENERAL INFORMATION:
;    APPLICANT:  Adermann, Knut
;    APPLICANT:  Hock, Dieter
;    APPLICANT:  Magerlein, Markus
;    TITLE OF INVENTION:  Peptides from the hPTH Sequence
;    NUMBER OF SEQUENCES:  36
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Jones & Askew, LLP
;      STREET:  191 Peachtree Street, 37th Floor
;      CITY:  Atlanta
;      STATE:  Georgia
;      COUNTRY:  USA
;      ZIP:  30303
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/817,547A
;      FILING DATE:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/EP95/03757
;      FILING DATE:  29 SEPT 1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  FROST, ROGER T.
;      REGISTRATION NUMBER:  22,176
;      REFERENCE/DOCKET NUMBER:  07826-0007
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  404-818-3700
;      TELEFAX:  404-818-3799
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  7 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  unknown
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  peptide
;    HYPOTHETICAL:  no
;    ANTI-SENSE:  no
US-08-817-547A-4

  Query Match             45.8%;  Score 27;  DB 3;  Length 7;
  Best Local Similarity   85.7%;  Pred. No. 3e+05;
  Matches    6;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AVSEIQL 7
              :||||||
Db          1 SVSEIQL 7


RESULT 11
US-08-428-257A-14
; Sequence 14, Application US/08428257A
; Patent No. 5885808
;  GENERAL INFORMATION:
;    APPLICANT:  Spooner, Robert A.
;    APPLICANT:  Epenetos, A.A.
;    TITLE OF INVENTION:  Compounds to target cells
;    NUMBER OF SEQUENCES:  80
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Jules E. Goldberg
;      STREET:  261 Madison Avenue
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10016-2391
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25 (EPO)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/428,257A
;      FILING DATE:  07/05/95
;      CLASSIFICATION:  514
;  INFORMATION FOR SEQ ID NO:  14:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-428-257A-14
```

```
  Query Match             42.4%;  Score 25;  DB 2;  Length 10;
  Best Local Similarity   83.3%;  Pred. No. 1.4e+02;
  Matches    5;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 VSEIQL 7
              |||:||
Db          4 VSEVQL 9


RESULT 12
US-08-802-981-124
; Sequence 124, Application US/08802981
; Patent No. 6037137
;  GENERAL INFORMATION:
;    APPLICANT:  Komoriya, Akira
;    APPLICANT:  Packard, Beverly S.
;    TITLE OF INVENTION:  Compositions for the Detection of Enzyme
;    TITLE OF INVENTION:  Activity in Biological Samples and Methods of Use Thereof
;    NUMBER OF SEQUENCES:  231
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew LLP
;      STREET:  Two Embarcadero Center, Eighth Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94111-3834
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/802,981
;      FILING DATE:  20-FEB-1997
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hunter, Tom
;      REGISTRATION NUMBER:  38,498
;      REFERENCE/DOCKET NUMBER:  016865-000300US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 576-0200
;      TELEFAX:  (415) 576-0300
;  INFORMATION FOR SEQ ID NO:  124:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  11 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  3
;      OTHER INFORMATION:  /product= "Aib"
US-08-802-981-124

  Query Match             42.4%;  Score 25;  DB 3;  Length 11;
  Best Local Similarity   80.0%;  Pred. No. 1.6e+02;
  Matches    4;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          6 QLMHN 10
              ||:||
Db          5 QLLHN 9


RESULT 13
US-08-177-109A-56
; Sequence 56, Application US/08177109A
; Patent No. 5869615
;  GENERAL INFORMATION:
;    APPLICANT:  Dennis E. Hourcade and Teresa J. Oglesby
;    TITLE OF INVENTION:  MODIFIED COMPLEMENT PROTEASES
;    NUMBER OF SEQUENCES:  62
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Patrea L. Pabst
;      STREET:  2800 One Atlantic Center
;      STREET:  1201 West Peachtree Street
;      CITY:  Atlanta
;      STATE:  Georgia
;      COUNTRY:  USA
;      ZIP:  30309-3450
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/177,109A
;      FILING DATE:  03-JAN-1994
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Pabst, Patrea L.
;      REGISTRATION NUMBER:  31,284
;      REFERENCE/DOCKET NUMBER:  WU 107
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (404) 873-8794
;      TELEFAX:  (404) 873-8795
;  INFORMATION FOR SEQ ID NO:  56:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  5 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    HYPOTHETICAL:  NO
US-08-177-109A-56

  Query Match             40.7%;  Score 24;  DB 2;  Length 5;
  Best Local Similarity   60.0%;  Pred. No. 3e+05;
  Matches    3;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 MHNLG 12
              :||:|
Db          1 LHNMG 5


RESULT 14
US-08-687-706-56
; Sequence 56, Application US/08687706
; Patent No. 5928892
;  GENERAL INFORMATION:
;    APPLICANT:  Dennis E. Hourcade and Teresa J. Oglesby
;    TITLE OF INVENTION:  MODIFIED COMPLEMENT PROTEASES
;    NUMBER OF SEQUENCES:  62
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Patrea L. Pabst
;      STREET:  2800 One Atlantic Center
;      STREET:  1201 West Peachtree Street
;      CITY:  Atlanta
;      STATE:  Georgia
;      COUNTRY:  USA
;      ZIP:  30309-3450
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/687,706
;      FILING DATE:  26-JUL-1996
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/177,109
;      FILING DATE:  03-JAN-1994
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Pabst, Patrea L.
```

```
;       REGISTRATION NUMBER:  31,284
;       REFERENCE/DOCKET NUMBER:  WU 107 DIV
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (404) 873-8794
;       TELEFAX:  (404) 873-8795
;   INFORMATION FOR SEQ ID NO:  56:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  5 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
;     HYPOTHETICAL:  NO
US-08-687-706-56

  Query Match             40.7%;  Score 24;  DB 2;  Length 5;
  Best Local Similarity   60.0%;  Pred. No. 3e+05;
  Matches    3;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 MHNLG 12
              :||:|
Db          1 LHNMG 5


RESULT 15
US-08-817-547A-17
; Sequence 17, Application US/08817547A
; Patent No. 6030790
;  GENERAL INFORMATION:
;     APPLICANT:  Adermann, Knut
;     APPLICANT:  Hock, Dieter
;     APPLICANT:  Magerlein, Markus
;     TITLE OF INVENTION:  Peptides from the hPTH Sequence
;     NUMBER OF SEQUENCES:  36
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Jones & Askew, LLP
;       STREET:  191 Peachtree Street, 37th Floor
;       CITY:  Atlanta
;       STATE:  Georgia
;       COUNTRY:  USA
;       ZIP:  30303
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/817,547A
;       FILING DATE:
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  PCT/EP95/03757
;       FILING DATE:  29 SEPT 1994
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  FROST, ROGER T.
;       REGISTRATION NUMBER:  22,176
;       REFERENCE/DOCKET NUMBER:  07826-0007
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  404-818-3700
;       TELEFAX:  404-818-3799
;   INFORMATION FOR SEQ ID NO:  17:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  5 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:  unknown
;       TOPOLOGY:  unknown
;     MOLECULE TYPE:  peptide
;     HYPOTHETICAL:  no
;     ANTI-SENSE:  no
US-08-817-547A-17

  Query Match             40.7%;  Score 24;  DB 3;  Length 5;
  Best Local Similarity   100.0%;  Pred. No. 3e+05;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          9 HNLG 12
              ||||
Db          1 HNLG 4


Search completed:  September  5, 2004, 09:38:33
Job time : 11 secs
```

OM protein - protein search, using sw model

Run on: September 5, 2004, 09:30:43 ; Search time 9.5 Seconds
(without alignments)
121.505 Million cell updates/sec

Title: US-09-730-174A-6
Perfect score: 61
Sequence: 1 AVSEIQFMHNLG 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 1581

Minimum DB seq length: 0
Maximum DB seq length: 12

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	20	32.8	10	2	S28055	cytochrome b559 co
2	20	32.8	12	2	PH1187	T-cell receptor al
3	18	29.5	7	2	A58718	carnocin UI49 - Ca
4	18	29.5	9	2	S78420	ribosomal protein
5	18	29.5	10	2	A60589	sperm-activating p
6	18	29.5	12	2	PH1190	T-cell receptor al
7	17	27.9	8	2	A05169	neuropeptide M-I -
8	17	27.9	10	2	A37268	Ig heavy chain C r
9	17	27.9	12	1	A43975	locustamyotropin -
10	17	27.9	12	2	S21205	Ig heavy chain V r
11	17	27.9	12	2	PH1189	T-cell receptor al
12	16	26.2	7	2	I46868	alpha-myosin heavy
13	16	26.2	10	2	JC1416	hypertrehalosemic
14	16	26.2	10	2	S09138	hypertrehalosemic
15	16	26.2	11	2	A32428	amine oxidase (cop
16	15	24.6	7	2	S29735	polyphosphate-gluc
17	15	24.6	9	2	PT0231	Ig heavy chain CDR
18	15	24.6	9	2	A56029	N-methylpurine DNA
19	15	24.6	10	2	S33844	alpha-2-macroglobu
20	15	24.6	10	2	S38304	lectin GNL1 alpha
21	15	24.6	10	2	E49033	T-cell receptor ga
22	15	24.6	11	2	A38841	rhodopsin homolog
23	15	24.6	12	2	A55837	5-aminoimidazole r
24	15	24.6	12	2	PH1174	T-cell receptor al
25	15	24.6	12	2	S51737	T-cell receptor be
26	14	23.0	4	2	A35779	neuropeptide Antho
27	14	23.0	7	2	S78024	ribosomal protein
28	14	23.0	8	2	S08995	hypertrehalosemic
29	14	23.0	8	2	A49823	adipokinetic hormo
30	14	23.0	8	2	A44960	neuropeptide Led-C
31	14	23.0	9	2	PW0002	chlorophyll a/b-bi
32	14	23.0	9	2	PT0238	Ig heavy chain CRD
33	14	23.0	10	1	SPPGNK	neuromedin K - pig
34	14	23.0	10	2	S27873	hypothetical prote
35	14	23.0	10	2	C61033	ranatachykinin C -
36	14	23.0	10	2	B46453	e antigen p20e pre
37	14	23.0	10	2	C44787	calliFMRFamide 12
38	14	23.0	11	2	B41835	translation elonga
39	14	23.0	11	2	S19301	endo-1,4-beta-xyla
40	14	23.0	11	2	PA0028	protein QA300042 -
41	14	23.0	11	2	S60354	retinal oxidase -
42	14	23.0	11	2	S53436	beta-D-galactosida
43	14	23.0	12	2	S25485	transcription fact
44	14	23.0	12	2	S71034	potB protein - Sal
45	14	23.0	12	2	PH1175	T-cell receptor al

ALIGNMENTS

RESULT 1
S28055
cytochrome b559 component psbF - pepper chloroplast (fragment)
C;Species: chloroplast Capsicum annuum (pepper)
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 11-Jun-1999
C;Accession: S28055
R;Kuntz, M.; Camara, B.; Weil, J.H.; Schantz, R.
Plant Mol. Biol. 20, 1185-1188, 1992
A;Title: The psbL gene from bell pepper (Capsicum annuum): plastid RNA editing also occ
A;Reference number: S28055; MUID:93099270; PMID:1463853
A;Accession: S28055
A;Molecule type: DNA
A;Residues: 1-10 <KUN>
A;Cross-references: EMBL:X65570; NID:g14344; PIDN:CAA46539.1; PID:g415734
C;Genetics:
A;Gene: psbF
A;Genome: chloroplast
C;Superfamily: cytochrome b559 component F
C;Keywords: chloroplast; photosynthesis; photosystem II; thylakoid

Query Match 32.8%; Score 20; DB 2; Length 10;
Best Local Similarity 37.5%; Pred. No. 7.4e+02;
Matches 3; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

```
Qy          1 AVSEIQFM 8
              ::| :||:
Db          1 SISAMQFI 8
```

RESULT 2
PH1187
T-cell receptor alpha chain V region (Cw3/1F11) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
C;Accession: PH1187
R;Casanova, J.L.; Cerottini, J.C.; Matthes, M.; Necker, A.; Gournier, H.; Barra, C.; Wi
J. Exp. Med. 176, 439-447, 1992
A;Title: H-2-restricted cytolytic T lymphocytes specific for HLA display T cell recepto
A;Reference number: S26512; MUID:92364546; PMID:1380061
A;Accession: PH1187
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-12 <CAS>

Query Match 32.8%; Score 20; DB 2; Length 12;
Best Local Similarity 71.4%; Pred. No. 9.1e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Qy          1 AVSEIQF 7
              ||||  |
Db          2 AVSETGF 8
```

RESULT 3
A58718
carnocin UI49 - Carnobacterium sp. (fragment)
C;Species: Carnobacterium sp.
C;Date: 23-Jan-1998 #sequence_revision 30-Jan-1998 #text_change 30-Jan-1998
C;Accession: A58718
R;Stoffels, G.; Nissen-Meyer, J.; Gudmundsdottir, A.; Sletten, K.; Holo, H.; Nes, I.F.
Appl. Environ. Microbiol. 58, 1417-1422, 1992
A;Title: Purification and characterization of a new bacteriocin isolated from a Carnobac
A;Reference number: A58718; MUID:92321768; PMID:1622206
A;Accession: A58718
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-7 <STO>
C;Keywords: antibiotic; lanthionine

Query Match 29.5%; Score 18; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SEIQ 6
||||
Db 2 SEIQ 5

RESULT 4
S78420
ribosomal protein RL41, mitochondrial [validated] - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 25-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 21-Jul-2000
C;Accession: S78420
R;Goldschmidt-Reisin, S.; Graack, H.R.
submitted to the Protein Sequence Database, February 1998
A;Reference number: S78411
A;Accession: S78420
A;Molecule type: protein
A;Residues: 1-9 <GOL>
A;Note: the protein is designated as mitochondrial ribosomal protein L41
C;Keywords: mitochondrion; protein biosynthesis; ribosome

Query Match 29.5%; Score 18; DB 2; Length 9;
Best Local Similarity 75.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 HNLG 12
| ||
Db 5 HRLG 8

RESULT 5
A60589
sperm-activating peptide (Tyr-2, Asn-3, Gly-5, Ile-9, Asp-10 SAP-I) - slate-pencil urchi
C;Species: Heterocentrotus mamillatus
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 18-Aug-2000
C;Accession: A60589
R;Yoshino, K.I.; Kajiura, H.; Nomura, K.; Takao, T.; Shimonishi, Y.; Kurita, M.; Yamaguc
Comp. Biochem. Physiol. B 94, 739-751, 1989
A;Title: A halogenated amino acid-containing sperm activating peptide and its related pe
otus nudus, Echinometra mathaei and Heterocentrotus mammillatus.
A;Reference number: A60527
A;Accession: A60589
A;Molecule type: protein
A;Residues: 1-10 <YOS>
C;Superfamily: unassigned animal peptides

Query Match 29.5%; Score 18; DB 2; Length 10;
Best Local Similarity 75.0%; Pred. No. 1.8e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 9 HNLG 12
:|||
Db 2 YNLG 5

RESULT 6
PH1190
T-cell receptor alpha chain V region (Cw3/10.1) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
C;Accession: PH1190
R;Casanova, J.L.; Cerottini, J.C.; Matthes, M.; Necker, A.; Gournier, H.; Barra, C.; Wid
J. Exp. Med. 176, 439-447, 1992
A;Title: H-2-restricted cytolytic T lymphocytes specific for HLA display T cell receptor
A;Reference number: S26512; MUID:92364546; PMID:1380061
A;Accession: PH1190
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-12 <CAS>

Query Match 29.5%; Score 18; DB 2; Length 12;
Best Local Similarity 71.4%; Pred. No. 2.3e+03;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AVSEIQF 7
|||| |
Db 2 AVSEHGF 8

RESULT 7
A05169
neuropeptide M-I - American cockroach
C;Species: Periplaneta americana (American cockroach)
C;Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 31-Dec-1993
C;Accession: A05169
R;Witten, J.L.; Schaffer, M.H.; O'Shea, M.; Cook, J.C.; Hemling, M.E.; Rinehart Jr., K.L
Biochem. Biophys. Res. Commun. 124, 350-358, 1984
A;Title: Structures of two cockroach neuropeptides assigned by fast atom bombardment mas
A;Reference number: A90118; MUID:85046530; PMID:6548628
A;Accession: A05169
A;Molecule type: protein
A;Residues: 1-8 <WIT>
C;Keywords: neuropeptide

Query Match 27.9%; Score 17; DB 2; Length 8;
Best Local Similarity 42.9%; Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 4 EIQFMHN 10
|: | |
Db 1 EVNFSPN 7

RESULT 8
A37268
Ig heavy chain C region (129) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 19-Mar-1997 #sequence_revision 13-Mar-1998 #text_change 13-Mar-1998
C;Accession: A37268
R;Ruff-Jamison, S.; Campos-Gonzalez, R.; Glenney Jr., J.R.
J. Biol. Chem. 266, 6607-6613, 1991
A;Title: Heavy and light chain variable region sequences and antibody properties of anti
A;Reference number: A38740; MUID:91177923; PMID:1706720
A;Accession: A37268
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-10 <RUF>

Query Match 27.9%; Score 17; DB 2; Length 10;
Best Local Similarity 44.4%; Pred. No. 2.9e+03;
Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 4 EIQFMHNLG 12
| | |:|
Db 1 ESQSFPNVG 9

```
RESULT 9
A43975
locustamyotropin - migratory locust
N;Alternate names: Lom-MT
C;Species: Locusta migratoria (migratory locust)
C;Date: 11-Feb-1993 #sequence_revision 02-Jun-1994 #text_change 08-Dec-1995
C;Accession: A43975
R;Schoofs, L.; Holman, G.M.; Hayes, T.K.; Tips, A.; Nachman, R.J.; Vandesande, F.; De Lo
Peptides 11, 427-433, 1990
A;Title: Isolation, identification and synthesis of locustamyotropin (Lom-MT), a novel h
A;Reference number: A43975; MUID:90341077; PMID:1974346
A;Accession: A43975
A;Molecule type: protein
A;Residues: 1-12 <SCH>
A;Note: the amino end of this peptide is not blocked
A;Note: synthetic locustamyotropin mimics natural locustamyotropin only in the amidated
C;Comment: This peptide was shown to stimulate visceral muscle contractions in locust ov
C;Superfamily: pyrokinin
C;Keywords: amidated carboxyl end; neuropeptide
F;12/Modified site: amidated carboxyl end (Leu) #status experimental

  Query Match             27.9%;  Score 17;  DB 1;  Length 12;
  Best Local Similarity   45.5%;  Pred. No. 3.5e+03;
  Matches    5;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 AVSEIQFMHNL 11
              ||   ||   |
Db          2 AVPAAQFSPRL 12


RESULT 10
S21205
Ig heavy chain V region - human
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 16-Aug-1996
C;Accession: S21205
R;Makiya, R.; Stigbrand, T.
Eur. J. Biochem. 205, 341-345, 1992
A;Title: Placental alkaline phosphatase has a binding site for the human immunoglobulin-
A;Reference number: S21205; MUID:92209522; PMID:1555592
A;Accession: S21205
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-12 <MAK>
C;Keywords: heterotetramer; immunoglobulin

  Query Match             27.9%;  Score 17;  DB 2;  Length 12;
  Best Local Similarity   33.3%;  Pred. No. 3.5e+03;
  Matches    3;  Conservative    3;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          4 EIQFMHNLG 12
              |:| : : |
Db          1 EVQLVESGG 9


RESULT 11
PH1189
T-cell receptor alpha chain V region (Cw3/2C3) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
C;Accession: PH1189
R;Casanova, J.L.; Cerottini, J.C.; Matthes, M.; Necker, A.; Gournier, H.; Barra, C.; Wid
J. Exp. Med. 176, 439-447, 1992
A;Title: H-2-restricted cytolytic T lymphocytes specific for HLA display T cell receptor
A;Reference number: S26512; MUID:92364546; PMID:1380061
A;Accession: PH1189
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-12 <CAS>

  Query Match             27.9%;  Score 17;  DB 2;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 3.5e+03;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AVSE 4
              ||||
Db          2 AVSE 5


RESULT 12
I46868
alpha-myosin heavy chain - rabbit (fragment)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 14-Feb-1997 #sequence_revision 14-Feb-1997 #text_change 05-Nov-1999
C;Accession: I46868
R;Friedman, D.J.; Umeda, P.K.; Sinha, A.M.; Hsu, H.
Proc. Natl. Acad. Sci. U.S.A. 81, 3044-3048, 1984
A;Title: Characterization of genomic clones specifying rabbit alpha- and beta-ventricul
A;Reference number: I46868; MUID:84221901; PMID:6328491
A;Accession: I46868
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-7 <FRI>
A;Cross-references: GB:K01698; NID:g165538; PIDN:AAA31415.1; PID:g165539

  Query Match             26.2%;  Score 16;  DB 2;  Length 7;
  Best Local Similarity   60.0%;  Pred. No. 2.8e+05;
  Matches    3;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          6 QFMHN 10
              | ||:
Db          1 QKMHD 5


RESULT 13
JC1416
hypertrehalosemic hormone I - stick insect (Carausius morosus)
N;Alternate names: neuropeptide Cam-HrTH-I
N;Contains: hypertrehalosemic factor II
C;Species: Carausius morosus
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C;Accession: JC1416; S07157
R;Gaede, G.; Kellner, R.; Rinehart, K.L.; Proefke, M.L.
Biochem. Biophys. Res. Commun. 189, 1303-1309, 1992
A;Title: A tryptophan-substituted member of the AKH/RPCH family isolated from a stick ir
A;Reference number: JC1416; MUID:93129188; PMID:1482345
A;Accession: JC1416
A;Molecule type: protein
A;Residues: 1-10 <GAE1>
R;Gaede, G.; Rinehart Jr., K.L.
Biol. Chem. Hoppe-Seyler 368, 67-75, 1987
A;Title: Primary structure of the hypertrehalosaemic factor II from the corpus cardiacu
A;Reference number: S07157; MUID:87157103; PMID:3828078
A;Accession: S07157
A;Molecule type: protein
A;Residues: 'Z',2-10 <GAE2>
C;Comment: Hypertrehalosemic factor II lacks the tryptophan modification.
C;Comment: This peptide raises hemolymph levels of trehalose in the cockroach Periplane
C;Superfamily: adipokinetic hormone
C;Keywords: amidated carboxyl end; glycoprotein; hormone; neuropeptide; pyroglutamic ac
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;8/Binding site: carbohydrate (Trp) (covalent) #status experimental
F;10/Modified site: amidated carboxyl end (Thr) #status experimental

  Query Match             26.2%;  Score 16;  DB 2;  Length 10;
  Best Local Similarity   33.3%;  Pred. No. 4.5e+03;
  Matches    3;  Conservative    2;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          4 EIQFMHNLG 12
              :: |   | |
Db          1 QLTFTPNWG 9


RESULT 14
S09138
```

hypertrehalosemic hormone II - stick insect (Extatosoma tiaratum)
N;Alternate names: Cam-HrTH-II
C;Species: Extatosoma tiaratum
C;Date: 30-Jun-1992 #sequence_revision 24-Oct-1997 #text_change 31-Oct-1997
C;Accession: S09138
R;Gaede, G.; Rinehart, K.L.
Biol. Chem. Hoppe-Seyler 371, 345-354, 1990
A;Title: Primary structures of hypertrehalosaemic neuropeptides isolated from the corpor
entalis and of the stick insect Extatosoma tiaratum assigned by tandem fast atom bombard
A;Reference number: S08995; MUID:90253659; PMID:2340112
A;Accession: S09138
A;Molecule type: protein
A;Residues: 1-10 <GAE>
A;Note: the amino-terminal residue forms pyrrolidone carboxylic acid; therefore, we have
C;Superfamily: adipokinetic hormone
C;Keywords: amidated carboxyl end; hormone; neuropeptide; pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;10/Modified site: amidated carboxyl end (Thr) #status experimental

  Query Match 26.2%; Score 16; DB 2; Length 10;
  Best Local Similarity 33.3%; Pred. No. 4.5e+03;
  Matches 3; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

```
Qy          4 EIQFMHNLG 12
              :: |   | |
Db          1 QLTFTPNWG 9
```

RESULT 15
A32428
amine oxidase (copper-containing) (EC 1.4.3.6) - pig (fragment)
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 12-Oct-1989 #sequence_revision 31-Dec-1993 #text_change 06-Sep-1996
C;Accession: A32428
R;van der Meer, R.A.; van Wassenaar, P.D.; van Brouwershaven, J.H.; Duine, J.A.
Biochem. Biophys. Res. Commun. 159, 726-733, 1989
A;Title: Primary structure of a pyrroloquinoline quinone (PQQ) containing peptide isolat
A;Reference number: A32428; MUID:89193662; PMID:2539124
A;Accession: A32428
A;Molecule type: protein
A;Residues: 1-7,'K',9-11 <VAN>
A;Note: the modified residue thought by the authors to be pyrroloquinoline quinone coval
C;Keywords: oxidoreductase; quinoprotein; topaquinone
F;8/Modified site: topaquinone (Tyr) #status predicted

  Query Match 26.2%; Score 16; DB 2; Length 11;
  Best Local Similarity 37.5%; Pred. No. 5e+03;
  Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

```
Qy          3 SEIQFMHN 10
              |:  | :|
Db          2 SDAVFTYN 9
```

Search completed: September 5, 2004, 09:37:44
Job time : 9.5 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: September 5, 2004, 09:27:07 ; Search time 6.5 Seconds
(without alignments)
96.130 Million cell updates/sec

Title: US-09-730-174A-6
Perfect score: 61
Sequence: 1 AVSEIQFMHNLG 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 501

Minimum DB seq length: 0
Maximum DB seq length: 12

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	20	32.8	10	1	PSBF_CAPAN	Q03367 capsicum an
2	18	29.5	7	1	LANC_CARUI	P36960 carnobacter
3	18	29.5	10	1	HTF1_ROMMI	P18110 romalea mic
4	17	27.9	12	1	LMT1_LOCMI	P22395 locusta mig
5	16	26.2	8	1	ALL6_CYDPO	P82157 cydia pomon
6	16	26.2	10	1	HTF2_CARMO	P11385 carausius m
7	15	24.6	5	1	EI03_LITRU	P82099 litoria rub
8	15	24.6	8	1	FUSS_FUSSO	P81010 fusarium so
9	15	24.6	11	1	EFG_CLOPA	P81350 clostridium
10	15	24.6	11	1	NUHM_CANFA	P49820 canis famil
11	14	23.0	4	1	FLRN_ANTEL	P58707 anthopleura
12	14	23.0	7	1	ALL7_CYDPO	P82158 cydia pomon
13	14	23.0	7	1	TY51_LITRU	P82065 litoria rub
14	14	23.0	8	1	AL18_CARMA	P81821 carcinus ma
15	14	23.0	8	1	ALL1_CYDPO	P82152 cydia pomon
16	14	23.0	8	1	HTF1_PERAM	P04548 periplaneta
17	14	23.0	9	1	FAR8_MACRS	P83281 macrobrachi
18	14	23.0	9	1	UF02_MOUSE	P38640 mus musculu
19	14	23.0	10	1	AL19_CARMA	P81822 carcinus ma
20	14	23.0	10	1	FAR2_PENMO	P83317 penaeus mon
21	14	23.0	10	1	FARC_CALVO	P41867 calliphora
22	14	23.0	10	1	TKNC_RANCA	P22690 rana catesb
23	14	23.0	10	1	TKNK_PIG	P01292 sus scrofa
24	14	23.0	11	1	ASL1_BACSE	P83146 bacteroides
25	14	23.0	12	1	PORD_METTM	P80903 methanobact
26	14	23.0	12	1	RS19_TOBBP	Q56251 tomato big
27	13	21.3	6	1	TRPI_PSEPU	P36414 pseudomonas
28	13	21.3	8	1	HTF_TENMO	P25419 tenebrio mo
29	13	21.3	8	1	LCK4_LEUMA	P21143 leucophaea
30	13	21.3	8	1	LCK6_LEUMA	P19988 leucophaea
31	13	21.3	9	1	CONO_CONGE	P05486 conus geogr
32	13	21.3	9	1	MOSH_CLYJA	P19852 clypeaster
33	13	21.3	9	1	OXYT_EISFO	P42998 eisenia foe
34	13	21.3	9	1	PPK1_PERAM	P82691 periplaneta
35	13	21.3	11	1	ASL2_BACSE	P83147 bacteroides
36	13	21.3	11	1	CORZ_PERAM	P11496 periplaneta
37	13	21.3	11	1	CSI5_BACSU	P81095 bacillus su
38	13	21.3	11	1	PVK1_PERAM	P41837 periplaneta
39	13	21.3	11	1	Q2OA_COMTE	P80464 comamonas t
40	13	21.3	12	1	UKA2_HUMAN	P31144 homo sapien
41	12	19.7	5	1	RE21_LITRU	P82071 litoria rub
42	12	19.7	5	1	RE31_LITRU	P82072 litoria rub
43	12	19.7	8	1	ANG2_BOTJA	Q10582 bothrops ja
44	12	19.7	8	1	HTF2_PERAM	P04549 periplaneta
45	12	19.7	9	1	FIBB_ERYPA	P19346 erythrocebu

ALIGNMENTS

```
RESULT 1
PSBF_CAPAN
ID   PSBF_CAPAN     STANDARD;      PRT;    10 AA.
AC   Q03367;
DT   01-JUN-1994 (Rel. 29, Created)
DT   01-JUN-1994 (Rel. 29, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Cytochrome b559 beta subunit (PSII reaction center subunit VI)
DE   (Fragment).
GN   PSBF.
OS   Capsicum annuum (Bell pepper).
OG   Chloroplast.
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC   lamiids; Solanales; Solanaceae; Capsicum.
OX   NCBI_TaxID=4072;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=cv. Lamuyo; TISSUE=Fruit, and Leaf;
RX   MEDLINE=93099270; PubMed=1463853;
RA   Kuntz M., Camara B., Weil J.-H., Schantz R.;
RT   "The psbL gene from bell pepper (Capsicum annuum): plastid RNA
RT   editing also occurs in non-photosynthetic chromoplasts.";
RL   Plant Mol. Biol. 20:1185-1188(1992).
CC   -!- FUNCTION: This b-type cytochrome is tightly associated with the
CC       reaction center of photosystem II and possibly is part of the
CC       water-oxidation complex.
CC   -!- SUBUNIT: Heterodimer of an alpha subunit and a beta subunit.
CC   -!- SIMILARITY: Belongs to the psbE / psbF family.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; X65570; CAA46539.1; -.
DR   PIR; S28055; S28055.
DR   HAMAP; MF_00643; -; 1.
DR   InterPro; IPR006216; Cyt_b559.
DR   PROSITE; PS00537; CYTOCHROME_B559; PARTIAL.
KW   Chloroplast; Photosystem II; Heme; Electron transport; Transmembrane.
FT   NON_TER       1      1
FT   TRANSMEM     <1      5       BY SIMILARITY.
FT   DOMAIN        6     10       LUMENAL (POTENTIAL).
SQ   SEQUENCE   10 AA;  1180 MW;  817D0F59D6D69DC5 CRC64;

  Query Match             32.8%;  Score 20;  DB 1;  Length 10;
  Best Local Similarity   37.5%;  Pred. No. 4.8e-02;
  Matches    3;  Conservative    4;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 AVSEIQFM 8
              ::| :||:
Db          1 SISAMQFI 8
```

```
RESULT 2
LANC_CARUI
ID   LANC_CARUI     STANDARD;      PRT;     7 AA.
AC   P36960;
DT   01-JUN-1994 (Rel. 29, Created)
DT   01-JUN-1994 (Rel. 29, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Lantibiotic carnocin UI49 (Fragment).
OS   Carnobacterium sp. (strain UI49).
OC   Bacteria; Firmicutes; Lactobacillales; Carnobacteriaceae;
OC   Carnobacterium.
OX   NCBI_TaxID=35782;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=92321768; PubMed=1622206;
RA   Stoffels G., Nissen-Meyer J., Gudmundsdottir A., Sletten K., Holo H.,
RA   Nes I.F.;
RT   "Purification and characterization of a new bacteriocin isolated from
RT   a Carnobacterium sp.";
RL   Appl. Environ. Microbiol. 58:1417-1422(1992).
CC   -!- FUNCTION: Lanthionine-containing peptide antibiotic (lantibiotic).
CC       Active on Gram-positive bacteria.
KW   Antibiotic; Bacteriocin; Lantibiotic.
FT   NON_TER       7      7
SQ   SEQUENCE   7 AA;  786 MW;  741776D05B05B810 CRC64;

  Query Match             29.5%;  Score 18;  DB 1;  Length 7;
  Best Local Similarity   100.0%;  Pred. No. 1.4e+05;
  Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 SEIQ 6
              ||||
Db          2 SEIQ 5


RESULT 3
HTF1_ROMMI
ID   HTF1_ROMMI     STANDARD;      PRT;     10 AA.
AC   P18110;
DT   01-NOV-1990 (Rel. 16, Created)
DT   01-FEB-1994 (Rel. 28, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   RO I (Hypertrehalosaemic factor).
OS   Romalea microptera (Lubber grasshopper).
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
OC   Acridoidea; Romaleidae; Romalea.
OX   NCBI_TaxID=7007;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Corpora cardiaca;
RX   MEDLINE=89145002; PubMed=3226948;
RA   Gaede G., Hilbich C., Beyreuther K., Rinehart K.L. Jr.;
RT   "Sequence analyses of two neuropeptides of the AKH/RPCH-family from
RT   the lubber grasshopper, Romalea microptera.";
RL   Peptides 9:681-688(1988).
CC   -!- FUNCTION: Hypertrehalosaemic factors are neuropeptides that
CC       elevate the level of trehalose in the hemolymph (trehalose is the
CC       major carbohydrate in the hemolymph of insects).
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: Belongs to the AKH / HRTH / RPCH family.
DR   InterPro; IPR002047; AKH.
DR   PROSITE; PS00256; AKH; 1.
KW   Neuropeptide; Amidation; Flight; Pyrrolidone carboxylic acid.
FT   MOD_RES       1      1       PYRROLIDONE CARBOXYLIC ACID.
FT   MOD_RES      10     10       AMIDATION.
SQ   SEQUENCE   10 AA;  1163 MW;  056236745771A9C4 CRC64;

  Query Match             29.5%;  Score 18;  DB 1;  Length 10;
  Best Local Similarity   33.3%;  Pred. No. 1.2e+03;
  Matches    3;  Conservative    2;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          4 EIQFMHNLG 12
              :: |  | ||
Db          1 QVNFTPNWG 9


RESULT 4
LMT1_LOCMI
ID   LMT1_LOCMI     STANDARD;      PRT;     12 AA.
AC   P22395;
DT   01-AUG-1991 (Rel. 19, Created)
DT   01-AUG-1991 (Rel. 19, Last sequence update)
DT   01-AUG-1991 (Rel. 19, Last annotation update)
DE   Locustamyotropin 1 (LOM-MT-1).
OS   Locusta migratoria (Migratory locust).
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
OC   Acridoidea; Acrididae; Oedipodinae; Locusta.
OX   NCBI_TaxID=7004;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Corpora cardiaca;
RX   MEDLINE=90341077; PubMed=1974346;
RA   Schoofs L., Holman G.M., Hayes T.K., Tips A., Nachman R.J.,
RA   Vandesande F., de Loof A.;
RT   "Isolation, identification and synthesis of locustamyotropin
RT   (Lom-MT), a novel biologically active insect peptide.";
RL   Peptides 11:427-433(1990).
CC   -!- FUNCTION: Mediates visceral muscle contractile activity (myotropic
CC       activity).
CC   -!- SIMILARITY: Belongs to the pyrokinin family.
DR   PIR; A43975; A43975.
DR   InterPro; IPR001484; Pyrokinin.
DR   PROSITE; PS00539; PYROKININ; 1.
KW   Neuropeptide; Amidation; Pyrokinin.
FT   MOD_RES      12     12       AMIDATION.
SQ   SEQUENCE   12 AA;  1213 MW;  D766C92722D6DDDD CRC64;

  Query Match             27.9%;  Score 17;  DB 1;  Length 12;
  Best Local Similarity   45.5%;  Pred. No. 2.3e+03;
  Matches    5;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 AVSEIQFMHNL 11
              ||  ||  |  |
Db          2 AVPAAQFSPRL 12


RESULT 5
ALL6_CYDPO
ID   ALL6_CYDPO     STANDARD;      PRT;     8 AA.
AC   P82157;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   Cydiastatin 6.
OS   Cydia pomonella (Codling moth).
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC   Tortricoidea; Tortricidae; Olethreutinae; Cydia.
OX   NCBI_TaxID=82600;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Larva;
RX   MEDLINE=98054539; PubMed=9392829;
RA   Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Winstanley D.,
RA   Davey M., East P.D., Thorpe A.;
RT   "Lepidopteran peptides of the allatostatin superfamily.";
RL   Peptides 18:1301-1309(1997).
CC   -!- SIMILARITY: Belongs to the allatostatin family.
KW   Neuropeptide; Amidation.
FT   MOD_RES       8      8       AMIDATION.
SQ   SEQUENCE   8 AA;  936 MW;  0B2879C45B573767 CRC64;
```

```
  Query Match             26.2%;  Score 16;  DB 1;  Length 8;
  Best Local Similarity   40.0%;  Pred. No. 1.4e+05;
  Matches    2;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          8 MHNLG 12
              ::| |
Db          3 LYNFG 7


RESULT 6
HTF2_CARMO
ID   HTF2_CARMO     STANDARD;      PRT;    10 AA.
AC   P11385;
DT   01-JUL-1989 (Rel. 11, Created)
DT   01-FEB-1994 (Rel. 28, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Hypertrehalosaemic factor II (HTF-II) (HRTH-II) (Hypertrehalosaemic
DE   neuropeptide II).
OS   Carausius morosus (Indian stick insect), and
OS   Extatosoma tiaratum (Stick insect).
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Orthopteroidea; Phasmatodea; Euphasmida; Phasmatoidea;
OC   Heteronemiidae; Carausius.
OX   NCBI_TaxID=7022, 7024;
RN   [1]
RP   SEQUENCE.
RC   SPECIES=C.morosus; TISSUE=Corpora cardiaca;
RX   MEDLINE=87157103; PubMed=3828078;
RA   Gaede G., Rinehart K.L. Jr.;
RT   "Primary structure of the hypertrehalosaemic factor II from the
RT   corpus cardiacum of the Indian stick insect, Carausius morosus,
RT   determined by fast atom bombardment mass spectrometry.";
RL   Biol. Chem. Hoppe-Seyler 368:67-75(1987).
RN   [2]
RP   SEQUENCE.
RC   SPECIES=E.tiaratum; TISSUE=Corpora cardiaca;
RX   MEDLINE=90253659; PubMed=2340112;
RA   Gaede G., Rinehart K.L. Jr.;
RT   "Primary structures of hypertrehalosaemic neuropeptides isolated from
RT   the corpora cardiaca of the cockroaches Leucophaea maderae,
RT   Gromphadorhina portentosa, Blattella germanica and Blatta orientalis
RT   and of the stick insect Extatosoma tiaratum assigned by tandem fast
RT   atom bombardment mass spectrometry.";
RL   Biol. Chem. Hoppe-Seyler 371:345-354(1990).
RN   [3]
RP   CARBOHYDRATE-LINKAGE SITE.
RC   SPECIES=C.morosus; TISSUE=Corpora cardiaca;
RX   MEDLINE=93129188; PubMed=1482345;
RA   Gaede G., Kellner R., Rinehart K.L. Jr., Proefke M.L.;
RT   "A tryptophan-substituted member of the AKH/RPCH family isolated from
RT   a stick insect corpus cardiacum.";
RL   Biochem. Biophys. Res. Commun. 189:1303-1309(1992).
CC   -!- FUNCTION: Hypertrehalosaemic factors are neuropeptides that
CC       elevate the level of trehalose in the hemolymph (trehalose is the
CC       major carbohydrate in the hemolymph of insects).
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- MASS SPECTROMETRY: MW=1308.61; METHOD=FAB.
CC   -!- SIMILARITY: Belongs to the AKH / HRTH / RPCH family.
DR   PIR; JC1416; JC1416.
DR   PIR; S09138; S09138.
DR   InterPro; IPR002047; AKH.
DR   PROSITE; PS00256; AKH; 1.
KW   Neuropeptide; Amidation; Glycoprotein; Pyrrolidone carboxylic acid.
FT   MOD_RES       1      1       PYRROLIDONE CARBOXYLIC ACID.
FT   CARBOHYD      8      8       C-LINKED (MAN) (PROBABLE).
FT   MOD_RES      10     10       AMIDATION.
SQ   SEQUENCE   10 AA;  1164 MW;  9B9036745771A9D1 CRC64;

  Query Match             26.2%;  Score 16;  DB 1;  Length 10;
  Best Local Similarity   33.3%;  Pred. No. 2.9e+03;
  Matches    3;  Conservative    2;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          4 EIQFMHNLG 12
                :: | | |
Db          1 QLTFTPNWG 9


RESULT 7
EI03_LITRU
ID   EI03_LITRU     STANDARD;      PRT;     5 AA.
AC   P82099;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Electrin 3.
OS   Litoria rubella (Desert tree frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae;
OC   Pelodryadinae; Litoria.
OX   NCBI_TaxID=104895;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Skin secretion;
RA   Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
RT   "Peptides from the skin glands of the Australian buzzing tree frog
RT   Litori electrica. Comparison with the skin peptides from Litoria
RT   rubella.";
RL   Aust. J. Chem. 52:639-645(1999).
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- TISSUE SPECIFICITY: Skin.
KW   Amphibian defense peptide; Amidation.
FT   MOD_RES       5      5       AMIDATION.
SQ   SEQUENCE   5 AA;  630 MW;  668761F2C9A00000 CRC64;

  Query Match             24.6%;  Score 15;  DB 1;  Length 5;
  Best Local Similarity   66.7%;  Pred. No. 1.4e+05;
  Matches    2;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 FMH 9
              |:|
Db          1 FVH 3


RESULT 8
FUSS_FUSSO
ID   FUSS_FUSSO     STANDARD;      PRT;     8 AA.
AC   P81010;
DT   15-JUL-1998 (Rel. 36, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Allergen Fus s I3596* (Fragment).
OS   Fusarium solani (subsp. pisi) (Nectria haematococca).
OC   Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC   Hypocreomycetidae; Hypocreales; Nectriaceae; Nectria.
OX   NCBI_TaxID=70791;
RN   [1]
RP   SEQUENCE.
RC   STRAIN=IARI 3596; TISSUE=Mycelium;
RA   Verma J., Gangal S.V.;
RL   Submitted (JUL-1997) to Swiss-Prot.
CC   -!- ALLERGEN: Causes an allergic reaction in human.
KW   Allergen.
FT   NON_TER       8      8
SQ   SEQUENCE   8 AA;  898 MW;  C372C441F5B69041 CRC64;

  Query Match             24.6%;  Score 15;  DB 1;  Length 8;
  Best Local Similarity   66.7%;  Pred. No. 1.4e+05;
  Matches    2;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          9 HNL 11
              ||:
Db          5 HNV 7


RESULT 9
EFG_CLOPA
```

```
ID   EFG_CLOPA      STANDARD;      PRT;    11 AA.
AC   P81350;
DT   15-JUL-1998 (Rel. 36, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Elongation factor G (EF-G) (CP 5) (Fragment).
GN   FUSA.
OS   Clostridium pasteurianum.
OC   Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC   Clostridium.
OX   NCBI_TaxID=1501;
RN   [1]
RP   SEQUENCE.
RC   STRAIN=W5;
RX   MEDLINE=98291870; PubMed=9629918;
RA   Flengsrud R., Skjeldal L.;
RT   "Two-dimensional gel electrophoresis separation and N-terminal
RT   sequence analysis of proteins from Clostridium pasteurianum W5.";
RL   Electrophoresis 19:802-806(1998).
CC   -!- FUNCTION: This protein promotes the GTP-dependent translocation of
CC       the nascent protein chain from the A-site to the P-site of the
CC       ribosome.
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC   -!- SIMILARITY: Belongs to the GTP-binding elongation factor family.
CC       EF-G/EF-2 subfamily.
DR   InterPro; IPR000795; EF_GTPbind.
DR   PROSITE; PS00301; EFACTOR_GTP; PARTIAL.
KW   Elongation factor; Protein biosynthesis; GTP-binding.
FT   NON_TER      11     11
SQ   SEQUENCE   11 AA;  1337 MW;  412E71F1D9C33B17 CRC64;

  Query Match             24.6%;  Score 15;  DB 1;  Length 11;
  Best Local Similarity   25.0%;  Pred. No. 5.1e+03;
  Matches    2;  Conservative    3;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          5 IQFMHNLG 12
              ::   |:|
Db          4 LEKFQNIG 11


RESULT 10
NUHM_CANFA
ID   NUHM_CANFA     STANDARD;      PRT;    11 AA.
AC   P49820;
DT   01-OCT-1996 (Rel. 34, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   NADH-ubiquinone oxidoreductase 24 kDa subunit (EC 1.6.5.3)
DE   (EC 1.6.99.3) (Fragment).
GN   NDUFV2.
OS   Canis familiaris (Dog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX   NCBI_TaxID=9615;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Heart;
RX   MEDLINE=98163340; PubMed=9504812;
RA   Dunn M.J., Corbett J.M., Wheeler C.H.;
RT   "HSC-2DPAGE and the two-dimensional gel electrophoresis database of
RT   dog heart proteins.";
RL   Electrophoresis 18:2795-2802(1997).
CC   -!- FUNCTION: TRANSFER OF ELECTRONS FROM NADH TO THE RESPIRATORY
CC       CHAIN. THE IMMEDIATE ELECTRON ACCEPTOR FOR THE ENZYME IS BELIEVED
CC       TO BE UBIQUINONE. COMPONENT OF THE FLAVOPROTEIN-SULFUR (FP)
CC       FRAGMENT OF THE ENZYME.
CC   -!- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
CC   -!- CATALYTIC ACTIVITY: NADH + acceptor = NAD(+) + reduced acceptor.
CC   -!- COFACTOR: Binds 1 2Fe-2S cluster (Potential).
CC   -!- SUBUNIT: Mammalian complex I is composed of 45 different subunits.
CC   -!- SUBCELLULAR LOCATION: Matrix and cytoplasmic side of the
CC       mitochondrial inner membrane.
CC   -!- SIMILARITY: Belongs to the complex I 24 kDa subunit family.
DR   HSC-2DPAGE; P49820; DOG.
DR   InterPro; IPR002023; Cmplx1_24kDa.
DR   PROSITE; PS01099; COMPLEX1_24K; PARTIAL.
KW   Oxidoreductase; NAD; Ubiquinone; Mitochondrion; Metal-binding;
KW   Iron-sulfur; Iron; 2Fe-2S.
FT   NON_TER      11     11
SQ   SEQUENCE   11 AA;  1099 MW;  267F5369C9C72DD8 CRC64;

  Query Match             24.6%;  Score 15;  DB 1;  Length 11;
  Best Local Similarity   66.7%;  Pred. No. 5.1e+03;
  Matches    2;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 FMH 9
              |:|
Db          7 FVH 9


RESULT 11
FLRN_ANTEL
ID   FLRN_ANTEL     STANDARD;      PRT;    4 AA.
AC   P58707;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Antho-RNamide.
OS   Anthopleura elegantissima (Sea anemone).
OC   Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actiniaria;
OC   Nynantheae; Actiniidae; Anthopleura.
OX   NCBI_TaxID=6110;
RN   [1]
RP   SEQUENCE, AND MASS SPECTROMETRY.
RX   MEDLINE=90319122; PubMed=1973541;
RA   Grimmelikhuijzen C.J.P., Rinehart K.L. Jr., Jacob E., Graff D.,
RA   Reinscheid R.K., Nothacker H.-P., Staley A.L.;
RT   "Isolation of L-3-phenyllactyl-Leu-Arg-Asn-NH2 (Antho-RNamide), a sea
RT   anemone neuropeptide containing an unusual amino-terminal blocking
RT   group.";
RL   Proc. Natl. Acad. Sci. U.S.A. 87:5410-5414(1990).
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- TISSUE SPECIFICITY: Neuron specific.
CC   -!- MASS SPECTROMETRY: MW=549.3; METHOD=FAB.
DR   PIR; A35779; A35779.
KW   Neuropeptide; Amidation.
FT   MOD_RES       1      1       L-3-PHENYLLACTYL.
FT   MOD_RES       4      4       AMIDATION.
SQ   SEQUENCE   4 AA;  549 MW;  64540729A0000000 CRC64;

  Query Match             23.0%;  Score 14;  DB 1;  Length 4;
  Best Local Similarity   50.0%;  Pred. No. 1.4e+05;
  Matches    2;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 FMHN 10
              |: |
Db          1 FLRN 4


RESULT 12
ALL7_CYDPO
ID   ALL7_CYDPO     STANDARD;      PRT;    7 AA.
AC   P82158;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   Cydiastatin 7.
OS   Cydia pomonella (Codling moth).
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC   Tortricoidea; Tortricidae; Olethreutinae; Cydia.
OX   NCBI_TaxID=82600;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Larva;
RX   MEDLINE=98054539; PubMed=9392829;
```

```
RA   Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Winstanley D.,
RA   Davey M., East P.D., Thorpe A.;
RT   "Lepidopteran peptides of the allatostatin superfamily.";
RL   Peptides 18:1301-1309(1997).
CC   -!- SIMILARITY: Belongs to the allatostatin family.
KW   Neuropeptide; Amidation.
FT   MOD_RES       7       7       AMIDATION.
SQ   SEQUENCE   7 AA;  873 MW;  672879CABB569350 CRC64;

  Query Match             23.0%;  Score 14;  DB 1;  Length 7;
  Best Local Similarity   40.0%;  Pred. No. 1.4e+05;
  Matches    2;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          8 MHNLG 12
              |:: |
Db          2 MYDFG 6


RESULT 13
TY51_LITRU
ID   TY51_LITRU     STANDARD;      PRT;     7 AA.
AC   P82065;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Tryptophyllin 5.1.
OS   Litoria rubella (Desert tree frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae;
OC   Pelodryadinae; Litoria.
OX   NCBI_TaxID=104895;
RN   [1]
RP   SEQUENCE, AND MASS SPECTROMETRY.
RC   TISSUE=Skin secretion;
RA   Steinborner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,
RA   Tyler M.J., Wallace J.C.;
RT   "The structure of new peptides from the Australin red tree frog
RT   'Litoria rubella'. The skin peptide profile as a probe for the study
RT   of evolutionary trends of amphibians.";
RL   Aust. J. Chem. 49:955-963(1996).
CC   -!- FUNCTION: May act as a neuromodulator or neurotransmitter.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.
CC   -!- MASS SPECTROMETRY: MW=965; METHOD=FAB.
KW   Amphibian defense peptide; Amidation; Neuropeptide;
KW   Pyrrolidone carboxylic acid.
FT   MOD_RES       1       1       PYRROLIDONE CARBOXYLIC ACID.
FT   MOD_RES       7       7       AMIDATION.
SQ   SEQUENCE   7 AA;  983 MW;  7401E9D3676046B0 CRC64;

  Query Match             23.0%;  Score 14;  DB 1;  Length 7;
  Best Local Similarity   33.3%;  Pred. No. 1.4e+05;
  Matches    2;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          4 EIQFMH 9
              :| : |
Db          1 QIPWFH 6


RESULT 14
AL18_CARMA
ID   AL18_CARMA     STANDARD;      PRT;     8 AA.
AC   P81821;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   Carcinustatin 18.
OS   Carcinus maenas (Common shore crab) (Green crab).
OC   Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC   Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC   Eubrachyura; Portunoidea; Portunidae; Carcinus.
OX   NCBI_TaxID=6759;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Cerebral ganglion, and Thoracic ganglion;
RX   MEDLINE=98121193; PubMed=9461295;
RA   Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
RA   Thorpe A.;
RT   "Isolation and identification of multiple neuropeptides of the
RT   allatostatin superfamily in the shore crab Carcinus maenas.";
RL   Eur. J. Biochem. 250:727-734(1997).
CC   -!- FUNCTION: May act as a neurotransmitter or neuromodulator.
CC   -!- SIMILARITY: Belongs to the allatostatin family.
KW   Neuropeptide; Amidation; Multigene family.
FT   MOD_RES       8       8       AMIDATION (POTENTIAL).
SQ   SEQUENCE   8 AA;  919 MW;  C82879D5AB569AB5 CRC64;

  Query Match             23.0%;  Score 14;  DB 1;  Length 8;
  Best Local Similarity   40.0%;  Pred. No. 1.4e+05;
  Matches    2;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          8 MHNLG 12
              |:: |
Db          3 MYSFG 7


RESULT 15
ALL1_CYDPO
ID   ALL1_CYDPO     STANDARD;      PRT;     8 AA.
AC   P82152;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   Cydiastatin 1.
OS   Cydia pomonella (Codling moth).
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC   Tortricoidea; Tortricidae; Olethreutinae; Cydia.
OX   NCBI_TaxID=82600;
RN   [1]
RP   SEQUENCE.
RC   TISSUE=Larva;
RX   MEDLINE=98054539; PubMed=9392829;
RA   Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Winstanley D.,
RA   Davey M., East P.D., Thorpe A.;
RT   "Lepidopteran peptides of the allatostatin superfamily.";
RL   Peptides 18:1301-1309(1997).
CC   -!- SIMILARITY: Belongs to the allatostatin family.
KW   Neuropeptide; Amidation.
FT   MOD_RES       8       8       AMIDATION.
SQ   SEQUENCE   8 AA;  934 MW;  C82879C45B51F775 CRC64;

  Query Match             23.0%;  Score 14;  DB 1;  Length 8;
  Best Local Similarity   50.0%;  Pred. No. 1.4e+05;
  Matches    2;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          9 HNLG 12
              :| |
Db          4 YNFG 7


Search completed: September  5, 2004, 09:35:03
Job time : 6.5 secs
```

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: September 5, 2004, 09:30:03 ; Search time 27.5 Seconds
(without alignments)
137.681 Million cell updates/sec

Title: US-09-730-174A-6
Perfect score: 61
Sequence: 1 AVSEIQFMHNLG 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 2565

Minimum DB seq length: 0
Maximum DB seq length: 12

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_25:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	24	39.3	11	13	Q9PS71	Q9ps71 agkistrodon
2	19	31.1	8	6	Q9TT78	Q9tt78 canis famil
3	19	31.1	9	12	O92766	O92766 canine dist
4	19	31.1	9	12	O71066	O71066 canine dist
5	19	31.1	12	13	P82081	P82081 limnodynast
6	18	29.5	8	3	O13591	O13591 saccharomyc
7	18	29.5	12	8	Q8MES0	Q8mes0 anoda crist
8	18	29.5	12	15	Q85631	Q85631 avian carci
9	17	27.9	11	5	Q23876	Q23876 dictyosteli
10	17	27.9	12	13	P82085	P82085 limnodynast
11	16	26.2	7	6	Q28742	Q28742 oryctolagus
12	16	26.2	8	3	Q05403	Q05403 saccharomyc
13	16	26.2	8	10	Q40659	Q40659 oryza sativ
14	16	26.2	8	13	P82082	P82082 limnodynast
15	16	26.2	8	13	P82083	P82083 limnodynast
16	16	26.2	9	2	Q44377	Q44377 aeromonas t
17	16	26.2	9	2	Q44468	Q44468 aeromonas v
18	16	26.2	9	2	Q8RKU3	Q8rku3 borrelia bu
19	16	26.2	9	2	Q43928	Q43928 aeromonas p
20	16	26.2	9	2	Q44001	Q44001 aeromonas e
21	16	26.2	9	10	Q9FXL0	Q9fxl0 lilium long
22	16	26.2	10	10	P82132	P82132 spinacia ol
23	16	26.2	10	10	P82133	P82133 spinacia ol
24	16	26.2	11	8	Q9GD68	Q9gd68 elaeis guin
25	16	26.2	11	10	P82336	P82336 pisum sativ
26	15	24.6	8	4	Q15894	Q15894 homo sapien
27	15	24.6	8	8	Q34909	Q34909 locusta mig
28	15	24.6	8	13	Q90493	Q90493 eopsaltria
29	15	24.6	9	2	Q43960	Q43960 azotobacter
30	15	24.6	9	4	Q15891	Q15891 homo sapien
31	15	24.6	9	10	Q8S3C6	Q8s3c6 glycine max
32	15	24.6	9	10	Q9FEC0	Q9fec0 hordeum vul
33	15	24.6	10	4	Q15342	Q15342 homo sapien
34	15	24.6	10	5	P82222	P82222 bombyx mori
35	15	24.6	10	10	Q8GZC8	Q8gzc8 hordeum vul
36	15	24.6	11	4	Q9C057	Q9c057 homo sapien
37	15	24.6	11	6	Q9BDC8	Q9bdc8 pongo pygma
38	15	24.6	11	6	Q9BDQ9	Q9bdq9 gorilla gor
39	15	24.6	11	6	Q9BDD0	Q9bdd0 pan troglod
40	15	24.6	11	6	Q9BDC9	Q9bdc9 pan paniscu
41	15	24.6	12	4	Q9UNV5	Q9unv5 homo sapien
42	14	23.0	7	8	O99182	O99182 gnatholebia
43	14	23.0	8	2	Q49534	Q49534 mycoplasma
44	14	23.0	8	12	Q84156	Q84156 orf virus (
45	14	23.0	8	13	Q91098	Q91098 manorina me

ALIGNMENTS

RESULT 1
Q9PS71
ID Q9PS71 PRELIMINARY; PRT; 11 AA.
AC Q9PS71;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Fibrinolytic metalloproteinase (Fragment).
OS Agkistrodon contortrix.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Agkistrodon.
OX NCBI_TaxID=8720;
RN [1]
RP SEQUENCE.
RX MEDLINE=91378546; PubMed=1898066;
RA Guan A.L., Retzios A.D., Henderson G.N., Markland F.S.Jr.;
RT "Purification and characterization of a fibrinolytic enzyme from venom
RT of the southern copperhead snake (Agkistrodon contortrix
RT contortrix).";
RL Arch. Biochem. Biophys. 289:197-207(1991).
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1209 MW; 7CA02D1D41E8772B CRC64;

Query Match 39.3%; Score 24; DB 13; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 HNLG 12
||||
Db 7 HNLG 10

RESULT 2
Q9TT78
ID Q9TT78 PRELIMINARY; PRT; 8 AA.
AC Q9TT78;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

```
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   Thymidylate synthase (Fragment).
GN   TS.
OS   Canis familiaris (Dog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX   NCBI_TaxID=9615;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21015404; PubMed=11130975;
RA   Brouillette J.A., Andrew J.R., Venta P.J.;
RT   "Estimate of nucleotide diversity in dogs with a pool-and-sequence
RT   method.";
RL   Mamm. Genome 11:1079-1086(2000).
DR   EMBL; AF202073; AAF20918.1; -.
FT   NON_TER       1      1
FT   NON_TER       8      8
SQ   SEQUENCE   8 AA;  899 MW;  6731A1E059CAA867 CRC64;

  Query Match             31.1%;  Score 19;  DB 6;  Length 8;
  Best Local Similarity   60.0%;  Pred. No. 1e+06;
  Matches    3;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 FMHNL 11
              |:| |
Db          4 FIHTL 8


RESULT 3
O92766
ID   O92766      PRELIMINARY;      PRT;     9 AA.
AC   O92766;
DT   01-NOV-1998 (TrEMBLrel. 08, Created)
DT   01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT   01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE   Fusion protein (Fragment).
GN   F.
OS   Canine distemper virus.
OC   Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC   Paramyxoviridae; Paramyxovirinae; Morbillivirus.
OX   NCBI_TaxID=11232;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Dog #5526/89;
RA   Liermann H., Harder T., Haas L.;
RT   "Genetic analysis of the central untranslated genome region and the
RT   proximal coding part of the F gene of wild-type and vaccine distemper
RT   morbilliviruses.";
RL   Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF026237; AAC09167.1; -.
FT   NON_TER       9      9
SQ   SEQUENCE   9 AA;  1011 MW;  F281732760533441 CRC64;

  Query Match             31.1%;  Score 19;  DB 12;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 1e+06;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 MHN 10
              |||
Db          1 MHN 3


RESULT 4
O71066
ID   O71066      PRELIMINARY;      PRT;     9 AA.
AC   O71066;
DT   01-AUG-1998 (TrEMBLrel. 07, Created)
DT   01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   Fusion protein (Fragment).
GN   F.
OS   Canine distemper virus.
OC   Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC   Paramyxoviridae; Paramyxovirinae; Morbillivirus.
OX   NCBI_TaxID=11232;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Dog #10757/96;
RA   Liermann H., Harder T., Haas L.;
RT   "Genetic analysis of the central untranslated genome region and the
RT   proximal coding part of the F gene of wild-type and vaccine distemper
RT   morbilliviruses.";
RL   Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF026234; AAC09164.1; -.
FT   NON_TER       9      9
SQ   SEQUENCE   9 AA;  1124 MW;  F29D045760440441 CRC64;

  Query Match             31.1%;  Score 19;  DB 12;  Length 9;
  Best Local Similarity   100.0%;  Pred. No. 1e+06;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 MHN 10
              |||
Db          1 MHN 3


RESULT 5
P82081
ID   P82081      PRELIMINARY;      PRT;    12 AA.
AC   P82081;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE   DYNASTIN 3.
OS   Limnodynastes terraereginae (Northen banjo frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Myobatrachidae;
OC   Limnodynastinae; Limnodynastes.
OX   NCBI_TaxID=104894;
RN   [1]
RP   SEQUENCE, AND MASS SPECTROMETRY.
RC   TISSUE=TIBIAL GLAND;
RA   Raftery M.J., Bradford A.M., Bowie J.H., Wallace J.C., Tyler M.J.;
RT   "Peptides from Australian frogs. The structure of the dynastins from
RT   the banjo frogs Limnodynastes interioras, Limnodynastes dumerilii and
RT   Limnodynastes terraereginae.";
RL   Aust. J. Chem. 46:833-842(1993).
CC   -!- MASS SPECTROMETRY: MW=1236; METHOD=FAB.
SQ   SEQUENCE   12 AA;  1236 MW;  147AA70FDF472724 CRC64;

  Query Match             31.1%;  Score 19;  DB 13;  Length 12;
  Best Local Similarity   60.0%;  Pred. No. 7.1e+03;
  Matches    3;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 MHNLG 12
              ::|||
Db          7 LNNLG 11


RESULT 6
O13591
ID   O13591      PRELIMINARY;      PRT;     8 AA.
AC   O13591;
DT   01-JAN-1998 (TrEMBLrel. 05, Created)
DT   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT   01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE   ORF YNL337W (Fragment).
OS   Saccharomyces cerevisiae (Baker's yeast).
OC   Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC   Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX   NCBI_TaxID=4932;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Obermaier B., Piravandi E., Rinke M.;
RL   Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
RN   [2]
```

```
RP   SEQUENCE FROM N.A.
RA   MIPS;
RL   Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; Z71612; CAA96271.2; -.
FT   NON_TER       1      1
SQ   SEQUENCE   8 AA;  1005 MW;  5CA441E449C9C720 CRC64;

  Query Match             29.5%;  Score 18;  DB 3;  Length 8;
  Best Local Similarity   75.0%;  Pred. No. 1e+06;
  Matches    3;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 FMHN 10
              | ||
Db          4 FNHN 7


RESULT 7
Q8MES0
ID   Q8MES0      PRELIMINARY;      PRT;    12 AA.
AC   Q8MES0;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Ribosomal protein 16 (Fragment).
GN   RPL16.
OS   Anoda cristata.
OG   Chloroplast.
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC   eurosids II; Malvales; Malvaceae; Malvoideae; Anoda.
OX   NCBI_TaxID=183227;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Pfeil B.E., Brubaker C.L., Craven L.A., Crisp M.D.;
RT   "Phylogeny of Hibiscus and the tribe Hibisceae (Malvaceae) using
RT   chloroplast DNA sequences of ndhF and the rpl16 intron.";
RL   Syst. Bot. 27:333-350(2002).
DR   EMBL; AF384567; AAM50405.1; -.
DR   GO; GO:0009507; C:chloroplast; IEA.
KW   Chloroplast.
FT   NON_TER       1      1
FT   NON_TER      12     12
SQ   SEQUENCE   12 AA;  1431 MW;  9A5E59B65452C9CA CRC64;

  Query Match             29.5%;  Score 18;  DB 8;  Length 12;
  Best Local Similarity   37.5%;  Pred. No. 1.1e+04;
  Matches    3;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          4 EIQFMHNL 11
              |  |::|:
Db          3 EPDFVNNI 10


RESULT 8
Q85631
ID   Q85631      PRELIMINARY;      PRT;    12 AA.
AC   Q85631;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   MH2, proviral DNA, myc to 3' LTR (Fragment).
OS   Avian carcinoma virus.
OC   Viruses; Retroid viruses; Retroviridae; Alpharetrovirus.
OX   NCBI_TaxID=11958;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=85033920; PubMed=6092695;
RA   Sutrave P., Jansen H.W., Bister K., Rapp U.R.;
RT   "3'-terminal region of avian carcinoma virus MH2 shares sequence
RT   elements with avian sarcoma viruses Y73 and SR-A.";
RL   J. Virol. 52:703-705(1984).
DR   EMBL; K03100; AAA42388.1; -.
FT   NON_TER       1      1
SQ   SEQUENCE   12 AA;  1466 MW;  72E4B884F30736DB CRC64;

  Query Match             29.5%;  Score 18;  DB 15;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 1.1e+04;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          9 HNL 11
              |||
Db          2 HNL 4


RESULT 9
Q23876
ID   Q23876      PRELIMINARY;      PRT;    11 AA.
AC   Q23876;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE   Actin 4.
OS   Dictyostelium discoideum (Slime mold).
OC   Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
OX   NCBI_TaxID=44689;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=82260445; PubMed=6286214;
RA   McKeown M., Firtel R.A.;
RT   "Actin multigene family of Dictyostelium.";
RL   Cold Spring Harb. Symp. Quant. Biol. 46:495-505(1982).
DR   EMBL; K02957; AAA33150.1; -.
DR   EMBL; K02956; AAA33150.1; JOINED.
SQ   SEQUENCE   11 AA;  1205 MW;  728B4C14C6C2CAAB CRC64;

  Query Match             27.9%;  Score 17;  DB 5;  Length 11;
  Best Local Similarity   28.6%;  Pred. No. 1.6e+04;
  Matches    2;  Conservative    4;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 EIQFMHN 10
              ::| ::|
Db          5 DVQALNN 11


RESULT 10
P82085
ID   P82085      PRELIMINARY;      PRT;    12 AA.
AC   P82085;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE   DYNASTIN 7.
OS   Limnodynastes salmini (Salmin's-striped frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Myobatrachidae;
OC   Limnodynastinae; Limnodynastes.
OX   NCBI_TaxID=39404;
RN   [1]
RP   SEQUENCE, AND MASS SPECTROMETRY.
RC   TISSUE=SKIN SECRETION;
RA   Bradford A.M., Raftery M.J., Bowie J.H., Wallace J.C., Tyler M.J.;
RT   "Peptides from Australian frogs. The structure of the dynastins from
RT   Limnodynastes salmini and Fletcherin from Limnodynastes fletcheri.";
RL   Aust. J. Chem. 46:1235-1244(1993).
CC   -!- MASS SPECTROMETRY: MW=1114; METHOD=FAB.
SQ   SEQUENCE   12 AA;  1114 MW;  3AB5A976CAA72728 CRC64;

  Query Match             27.9%;  Score 17;  DB 13;  Length 12;
  Best Local Similarity   50.0%;  Pred. No. 1.8e+04;
  Matches    6;  Conservative    2;  Mismatches    2;  Indels    2;  Gaps    1;

Qy          1 AVSEIQFMHNLG 12
              ||| :  : |||
Db          2 AVSGL--LTNLG 11
```

```
RESULT 11
Q28742
ID   Q28742      PRELIMINARY;      PRT;     7 AA.
AC   Q28742;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Alpha-myosin heavy chain (Fragment).
OS   Oryctolagus cuniculus (Rabbit).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX   NCBI_TaxID=9986;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=84221901; PubMed=6328491;
RA   Friedman D.J., Umeda P.K., Sinha A.M., Hsu H.-J., Jokovcic S.,
RA   Rabinowitz M.;
RT   "Characterization of genomic clones specifying rabbit alpha- and beta-
RT   ventricular myosin heavy chains.";
RL   Proc. Natl. Acad. Sci. U.S.A. 81:3044-3048(1984).
DR   EMBL; K01698; AAA31415.1; -.
DR   PIR; I46868; I46868.
FT   NON_TER       1       1
SQ   SEQUENCE   7 AA;  916 MW;  6B1B1AA1E69326B0 CRC64;

  Query Match             26.2%;  Score 16;  DB 6;  Length 7;
  Best Local Similarity   60.0%;  Pred. No. 1e+06;
  Matches    3;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          6 QFMHN 10
              | ||:
Db          1 QKMHD 5


RESULT 12
Q05403
ID   Q05403      PRELIMINARY;      PRT;     8 AA.
AC   Q05403;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE   DNA for ORF'S from chromosome XV (Fragment).
OS   Saccharomyces cerevisiae (Baker's yeast).
OC   Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC   Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX   NCBI_TaxID=4932;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=FY1679;
RX   MEDLINE=96021609; PubMed=8533473;
RA   Zumstein E., Pearson B.M., Kalogeropoulos A., Schweizer M.;
RT   "A 29.425 kb segment on the left arm of yeast chromosome XV contains
RT   more than twice as many unknown as known open reading frames.";
RL   Yeast 11:975-986(1995).
DR   EMBL; X83121; CAA58183.1; -.
FT   NON_TER       8       8
SQ   SEQUENCE   8 AA;  879 MW;  7B5322D2C441E058 CRC64;

  Query Match             26.2%;  Score 16;  DB 3;  Length 8;
  Best Local Similarity   50.0%;  Pred. No. 1e+06;
  Matches    2;  Conservative    2;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 MHNL 11
              :||:
Db          2 IHNV 5


RESULT 13
Q40659
ID   Q40659      PRELIMINARY;      PRT;     8 AA.
AC   Q40659;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE   Alpha-amylase (Fragment).
OS   Oryza sativa (Rice).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC   Ehrhartoideae; Oryzeae; Oryza.
OX   NCBI_TaxID=4530;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91078641; PubMed=2258052;
RA   Kumagai M.H., Shah M., Terashima M., Vrkljan Z., Whitaker J.R.,
RA   Rodriquez R.L.;
RT   "Expression and secretion of rice alpha-amylase by saccharomycers
RT   cerevisiae.";
RL   Gene 94:209-216(1990).
DR   EMBL; M62916; AAA33892.1; -.
DR   Gramene; Q40659; -.
FT   NON_TER       8       8
SQ   SEQUENCE   8 AA;  948 MW;  EBC694444732D6D6 CRC64;

  Query Match             26.2%;  Score 16;  DB 10;  Length 8;
  Best Local Similarity   28.6%;  Pred. No. 1e+06;
  Matches    2;  Conservative    4;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          5 IQFMHNL 11
              :| ::|:
Db          1 MQVLNNM 7


RESULT 14
P82082
ID   P82082      PRELIMINARY;      PRT;     8 AA.
AC   P82082;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE   DYNASTIN 4.
OS   Limnodynastes salmini (Salmin's-striped frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Myobatrachidae;
OC   Limnodynastinae; Limnodynastes.
OX   NCBI_TaxID=39404;
RN   [1]
RP   SEQUENCE, AND MASS SPECTROMETRY.
RC   TISSUE=SKIN SECRETION;
RA   Bradford A.M., Raftery M.J., Bowie J.H., Wallace J.C., Tyler M.J.;
RT   "Peptides from Australian frogs. The structure of the dynastins from
RT   Limnodynastes salmini and Fletcherin from Limnodynastes fletcheri.";
RL   Aust. J. Chem. 46:1235-1244(1993).
CC   -!- MASS SPECTROMETRY: MW=772; METHOD=FAB.
SQ   SEQUENCE   8 AA;  772 MW;  7B58772455A2C728 CRC64;

  Query Match             26.2%;  Score 16;  DB 13;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 1e+06;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         10 NLG 12
              |||
Db          5 NLG 7


RESULT 15
P82083
ID   P82083      PRELIMINARY;      PRT;     8 AA.
AC   P82083;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE   DYNASTIN 5.
OS   Limnodynastes salmini (Salmin's-striped frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Myobatrachidae;
OC   Limnodynastinae; Limnodynastes.
```

```
OX   NCBI_TaxID=39404;
RN   [1]
RP   SEQUENCE, AND MASS SPECTROMETRY.
RC   TISSUE=SKIN SECRETION;
RA   Bradford A.M., Raftery M.J., Bowie J.H., Wallace J.C., Tyler M.J.;
RT   "Peptides from Australian frogs. The structure of the dynastins from
RT   Limnodynastes salmini and Fletcherin from Limnodynastes fletcheri.";
RL   Aust. J. Chem. 46:1235-1244(1993).
CC   -!- MASS SPECTROMETRY: MW=786; METHOD=FAB.
SQ   SEQUENCE   8 AA;  786 MW;  7B58772455B05728 CRC64;

  Query Match             26.2%;  Score 16;  DB 13;  Length 8;
  Best Local Similarity   100.0%;  Pred. No. 1e+06;
  Matches    3;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         10 NLG 12
              |||
Db          5 NLG 7


Search completed: September  5, 2004, 09:37:01
Job time : 28.5 secs
```

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: September 5, 2004, 09:26:47 ; Search time 36.5 Seconds
(without alignments)
92.892 Million cell updates/sec

Title: US-09-730-174A-6
Perfect score: 61
Sequence: 1 AVSEIQFMHNLG 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 368311

Minimum DB seq length: 0
Maximum DB seq length: 12

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	50	82.0	11	6	ABG72607	Abg72607 Parathyro
2	50	82.0	12	6	ABG72608	Abg72608 Parathyro
3	49	80.3	11	3	AAY96968	Aay96968 Parathyro
4	42	68.9	10	2	AAR91644	Aar91644 Human par
5	42	68.9	10	3	AAY68767	Aay68767 Amino aci
6	42	68.9	10	4	AAB86219	Aab86219 Human par
7	42	68.9	10	6	ABR44166	Abr44166 Human par
8	41.5	68.0	11	2	AAY50600	Aay50600 Resin bou
9	41	67.2	9	4	AAB86225	Aab86225 Human par
10	39	63.9	9	3	AAB01862	Aab01862 PTH(1-14)
11	39	63.9	9	3	AAY96966	Aay96966 Parathyro
12	36	59.0	9	2	AAR91645	Aar91645 Human par
13	36	59.0	9	3	AAB01863	Aab01863 PTH(1-14)
14	36	59.0	9	3	AAY96981	Aay96981 Parathyro
15	36	59.0	9	4	AAB86220	Aab86220 Human par
16	36	59.0	10	4	AAB96932	Aab96932 Rat parat
17	36	59.0	11	4	AAB96931	Aab96931 Rat parat
18	36	59.0	11	4	AAB96915	Aab96915 Parathyro
19	36	59.0	11	4	AAB84770	Aab84770 Parathyro
20	36	59.0	12	4	AAB96914	Aab96914 Parathyro
21	36	59.0	12	4	AAB84769	Aab84769 Parathyro
22	34	55.7	12	2	AAW45785	Aaw45785 Parathyro
23	31	50.8	10	6	ABP71484	Abp71484 Parathyro
24	31	50.8	11	1	AAP82547	Aap82547 (Asn10, T
25	31	50.8	11	4	AAB96892	Aab96892 Rat parat
26	31	50.8	11	6	ABP71485	Abp71485 Parathyro
27	31	50.8	11	6	ABP71483	Abp71483 Parathyro
28	31	50.8	12	4	AAB96891	Aab96891 Rat parat
29	31	50.8	12	6	ABP71482	Abp71482 Parathyro
30	29	47.5	9	3	AAB01864	Aab01864 PTH(1-14)
31	29	47.5	9	3	AAY78849	Aay78849 Parathyro
32	29	47.5	9	3	AAY97062	Aay97062 PTH-rP N-
33	28	45.9	8	2	AAR91646	Aar91646 Human par
34	28	45.9	8	3	AAB07467	Aab07467 Antigenic
35	28	45.9	8	4	AAB86221	Aab86221 Human par
36	27	44.3	10	4	AAG63991	Aag63991 Complemen
37	27	44.3	11	4	ABU54029	Abu54029 Human DNA
38	27	44.3	12	2	AAR90421	Aar90421 Antibody
39	27	44.3	12	2	AAY55148	Aay55148 Anti CD34
40	27	44.3	12	3	AAY86894	Aay86894 Human hae
41	26	42.6	7	3	AAB00068	Aab00068 N-termina
42	26	42.6	9	3	AAB01866	Aab01866 PTH(1-14)
43	25	41.0	9	6	ABP83654	Abp83654 HLA prote
44	25	41.0	9	6	ABP89380	Abp89380 HLA prote
45	25	41.0	9	6	ABP88771	Abp88771 HLA prote

ALIGNMENTS

RESULT 1
ABG72607
ID ABG72607 standard; peptide; 11 AA.
XX
AC ABG72607;
XX
DT 11-FEB-2003 (first entry)
XX
DE Parathyroid hormone antigenic peptide 2-12.
XX
KW Human; parathyroid hormone; antigen; hypercalcaemia; osteoporosis;
KW primary hyperparathyroidism; mouse; rat; bovine; porcine; canine.
XX
OS Homo sapiens.
OS Mus sp.
OS Rattus sp.
OS Bos taurus.
OS Sus scrofa.
OS Canis familiaris.
XX
FH Key Location/Qualifiers
FT Misc-difference 6
FT /label= Leu, Phe
XX
PN US2002110871-A1.
XX
PD 15-AUG-2002.
XX
PF 05-DEC-2000; 2000US-00730174.
XX
PR 05-DEC-2000; 2000US-00730174.
XX
PA (ZAHR/) ZAHRADNIK R J.
PA (LAVI/) LAVIGNE J R.
XX
PI Zahradnik RJ, Lavigne JR;
XX
DR WPI; 2003-066685/06.
XX
PT New parathyroid hormone (PTH) antigenic peptide inducing the formation
PT and isolation of antibodies having an affinity to it, useful for
PT determining bioactive PTH levels in serum, plasma and/or cell culture
PT media.
XX
PS Claim 1; Page 5; 11pp; English.
XX
CC The invention relates to a new antigenic peptide for inducing the
CC formation and isolation of antibodies having an affinity to it, being

CC formed from the N-terminus of parathyroid hormone (PTH). Also included
CC are; (1) a method for producing antibodies useful in the determination of
CC PTH levels in a biological sample comprising: (a) providing at least one
CC first peptide antigen comprising a peptide fragment of PTH; (b)
CC administering the first peptide antigen to a host animal to induce
CC antibody production; (c) monitoring the antibody titre produced; (d)
CC isolating antisera produced in the host animal; and (e) selecting
CC antisera from the isolated antisera produced in the host that is capable
CC of binding to a second peptide antigen; (2) an antibody (ab) produced by
CC the method; and (3) test kits and analytical procedures used for the
CC determination of bioactive intact PTH utilising (ab). The methods and
CC compositions of the present invention are useful for determining
CC bioactive intact PTH levels in serum, plasma and/or cell culture media.
CC The antigens, antibodies and methods of the present invention, as
CC compared to prior art, have the particular advantages of possessing
CC greater affinity for PTH, and in particular, are designed to have a novel
CC recognition for amino acid residues extending beyond the first N-terminal
CC PTH residue, and further have negligible cross-reactivity with the large
CC non-molecular forms of PTH. PTH levels are an important parameter in
CC patients suffering from hypercalcaemia, osteoporosis and primary
CC hyperparathyroidism. The present sequence represents a PTH antigenic
CC peptide representing amino acids 2-12 of human, mouse, rat, porcine,
CC canine and bovine PTH
XX
SQ Sequence 11 AA;

Query Match 82.0%; Score 50; DB 6; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.013;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 VSEIQFMHNLG 12
||||| |||||
Db 1 VSEIQXMHNLG 11

RESULT 2
ABG72608
ID ABG72608 standard; peptide; 12 AA.
XX
AC ABG72608;
XX
DT 11-FEB-2003 (first entry)
XX
DE Parathyroid hormone antigenic peptide 1-12.
XX
KW Human; parathyroid hormone; antigen; hypercalcaemia; osteoporosis;
KW primary hyperparathyroidism; mouse; rat; bovine; porcine; canine.
XX
OS Homo sapiens.
OS Mus sp.
OS Rattus sp.
OS Bos taurus.
OS Sus scrofa.
OS Canis familiaris.
XX
FH Key Location/Qualifiers
FT Misc-difference 1
FT /label= Ser, Ala
FT Misc-difference 7
FT /label= Leu, Phe
XX
PN US2002110871-A1.
XX
PD 15-AUG-2002.
XX
PF 05-DEC-2000; 2000US-00730174.
XX
PR 05-DEC-2000; 2000US-00730174.
XX
PA (ZAHR/) ZAHRADNIK R J.
PA (LAVI/) LAVIGNE J R.
XX
PI Zahradnik RJ, Lavigne JR;
XX
DR WPI; 2003-066685/06.
XX
PT New parathyroid hormone (PTH) antigenic peptide inducing the formation
PT and isolation of antibodies having an affinity to it, useful for
PT determining bioactive PTH levels in serum, plasma and/or cell culture
PT media.
XX
PS Claim 2; Page 5; 11pp; English.
XX
CC The invention relates to a new antigenic peptide for inducing the
CC formation and isolation of antibodies having an affinity to it, being
CC formed from the N-terminus of parathyroid hormone (PTH). Also included
CC are; (1) a method for producing antibodies useful in the determination of
CC PTH levels in a biological sample comprising: (a) providing at least one
CC first peptide antigen comprising a peptide fragment of PTH; (b)
CC administering the first peptide antigen to a host animal to induce
CC antibody production; (c) monitoring the antibody titre produced; (d)
CC isolating antisera produced in the host animal; and (e) selecting
CC antisera from the isolated antisera produced in the host that is capable
CC of binding to a second peptide antigen; (2) an antibody (ab) produced by
CC the method; and (3) test kits and analytical procedures used for the
CC determination of bioactive intact PTH utilising (ab). The methods and
CC compositions of the present invention are useful for determining
CC bioactive intact PTH levels in serum, plasma and/or cell culture media.
CC The antigens, antibodies and methods of the present invention, as
CC compared to prior art, have the particular advantages of possessing
CC greater affinity for PTH, and in particular, are designed to have a novel
CC recognition for amino acid residues extending beyond the first N-terminal
CC PTH residue, and further have negligible cross-reactivity with the large
CC non-molecular forms of PTH. PTH levels are an important parameter in
CC patients suffering from hypercalcaemia, osteoporosis and primary
CC hyperparathyroidism. The present sequence represents a PTH antigenic
CC peptide representing amino acids 1-12 of human, mouse, rat, porcine,
CC canine and bovine PTH
XX
SQ Sequence 12 AA;

Query Match 82.0%; Score 50; DB 6; Length 12;
Best Local Similarity 90.9%; Pred. No. 0.014;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 VSEIQFMHNLG 12
||||| |||||
Db 2 VSEIQXMHNLG 12

RESULT 3
AAY96968
ID AAY96968 standard; peptide; 11 AA.
XX
AC AAY96968;
XX
DT 31-OCT-2000 (first entry)
XX
DE Parathyroid hormone N-terminal signaling domain (residues 1-11).
XX
KW PTH; parathyroid hormone; N-terminal; signaling domain; bone mass;
KW bone reformation; resorption; remodeling; tether1; osteoporosis.
XX
OS Homo sapiens.
XX
PN WO200039278-A2.
XX
PD 06-JUL-2000.
XX
PF 30-DEC-1999; 99WO-US031108.
XX
PR 31-DEC-1998; 98US-0114577P.
XX
PA (GARD/) GARDELLA T J.
PA (KRON/) KRONENBERG H M.
PA (POTT/) POTTS J T.

PA (JUEP/) JUEPPNER H.
XX
PI Gardella TJ, Kronenberg HM, Potts JT, Jueppner H;
XX
DR WPI; 2000-452384/39.
XX
PT New compound comprising an amino terminal signaling functional domain
PT linked to a carboxy-terminal binding portion of parathyroid hormone for
PT treating mammalian conditions characterized by decreases in bone mass.
XX
PS Claim 4; Page 92; 119pp; English.
XX
CC Compounds of the structure or formula S-(L)_n-B, R_1-S-(L)_n-R or S-(L)_n
CC -R, are new. S is an amino terminal signaling functional domain of
CC parathyroid hormone (PTH); L is a linker molecule present n times (where
CC n is a positive integer 1-10 (preferably 4)); B is a C-terminal binding
CC portion of PTH(1-34) or a PTH-related protein (PTH-rP) (1-34); R_1 is the
CC PTH-1 receptor signal sequence; and R is (a portion of) PTH-1 receptor
CC sequence. The new compounds are used for treating mammalian conditions
CC characterized by decreases in bone mass, determining rates of bone
CC reformation, bone resorption and/or bone remodeling, treating diseases
CC and disorders associated with decreased tetherl activity, increasing cAMP
CC in a mammalian cell having PTH-1 receptors, or screening for a peptide or
CC non-peptide PTH (claimed). The new compound can be administered by
CC inhalation unlike the large native PTH or PTHrP which avoids the need for
CC regular injections to treat osteoporosis
XX
SQ Sequence 11 AA;

Query Match 80.3%; Score 49; DB 3; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.02;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AVSEIQFMHNL 11
||||||| ||||
Db 1 AVSEIQLMHNL 11

RESULT 4
AAR91644
ID AAR91644 standard; peptide; 10 AA.
XX
AC AAR91644;
XX
DT 06-NOV-1996 (first entry)
XX
DE Human parathyroid hormone antigenic peptide hPTH 1-10.
XX
KW Human parathyroid hormone; hPTH; antigen; alpha-helix; immunogen;
KW diagnosis; active hPTH 1-37.
XX
OS Synthetic.
XX
PN DE4434551-A1.
XX
PD 04-APR-1996.
XX
PF 28-SEP-1994; 94DE-04434551.
XX
PR 28-SEP-1994; 94DE-04434551.
XX
PA (FORS/) FORSSMANN W.
XX
PI Adermann K, Forssmann W, Hock D, Maegerlein M;
XX
DR WPI; 1996-180391/19.
XX
PT New antigenic peptide(s) from human parathyroid hormone - and antibodies
PT generated using them, able to distinguish between active and inactive
PT forms of the hormone.
XX
PS Claim 2; Page 4; 5pp; German.
XX
CC The present sequence is a specific example of claimed immunogenic
CC peptides having a sequence from hPTH(1-37) which includes the N- or C-
CC terminal alpha-helical region and/or the non-structured region of the
CC hormone. Antibodies and their binding fragments generated by injecting an
CC animal with the peptides are useful as diagnostic reagents for
CC determination of biologically active hPTH(1-37)
XX
SQ Sequence 10 AA;

Query Match 68.9%; Score 42; DB 2; Length 10;
Best Local Similarity 80.0%; Pred. No. 0.37;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AVSEIQFMHN 10
:||||| |||
Db 1 SVSEIQLMHN 10

RESULT 5
AAY68767
ID AAY68767 standard; peptide; 10 AA.
XX
AC AAY68767;
XX
DT 05-MAY-2000 (first entry)
XX
DE Amino acids 1-10 of a parathyroid hormone (pTH).
XX
KW Parathyroid hormone; lipolysis; cosmetic; dermatological; skin care;
KW slimming treatment; cellulite; skin firming.
XX
OS Unidentified.
XX
PN WO200004047-A1.
XX
PD 27-JAN-2000.
XX
PF 07-JUL-1999; 99WO-FR001687.
XX
PR 17-JUL-1998; 98FR-00009193.
XX
PA (SEDE-) SEDERMA.
XX
PI Lintner K;
XX
DR WPI; 2000-171243/15.
XX
PT New parathyroid hormone fragment peptides, used as lipolysis stimulants
PT in topically applied cosmetic compositions for slimming treatment of
PT excessive weight in hips and thighs.
XX
PS Claim 1; Page 8; 18pp; French.
XX
CC The present sequence represents a parathyroid hormone (pTH) fragment,
CC comprising amino acids 1-10. Parathyroid hormone fragments of the
CC invention have lipolysis stimulating activity (especially when topically
CC administered). The lipolytic activity of the peptides is enhanced when
CC they are chemically modified to increase their lipophilicity. The
CC peptides are used in cosmetic or dermatological compositions for skin
CC care. They are especially used for slimming treatment of excessive weight
CC in the thighs and hips, in the treatment of cellulite and for skin
CC firming
XX
SQ Sequence 10 AA;

Query Match 68.9%; Score 42; DB 3; Length 10;
Best Local Similarity 80.0%; Pred. No. 0.37;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AVSEIQFMHN 10
:||||| |||
Db 1 SVSEIQLMHN 10

```
RESULT 6
AAB86219
ID   AAB86219 standard; peptide; 10 AA.
XX
AC   AAB86219;
XX
DT   03-SEP-2001  (first entry)
XX
DE   Human parathyroid hormone immunogenic peptide SEQ ID 1.
XX
KW   Parathyroid hormone; hPTH; immunogenic peptide; human; epitope;
KW   diagnosis; calcium-metabolism disorder; osteopathy; antagonist;
KW   hypo-parathyroidism; hyper-parathyroidism.
XX
OS   Homo sapiens.
XX
PN   DE19961350-A1.
XX
PD   21-JUN-2001.
XX
PF   17-DEC-1999;   99DE-01061350.
XX
PR   17-DEC-1999;   99DE-01061350.
XX
PA   (IMMU-) IMMUNDIAGNOSTIK AG.
XX
PI   Armbruster FP;
XX
DR   WPI; 2001-376318/40.
XX
PT   Determining the content of physiologically active parathyroid hormone,
PT   useful in diagnosis of calcium-metabolism disorders, using two antibodies
PT   reactive with different epitopes.
XX
PS   Disclosure; Page 3; 10pp; German.
XX
CC   This invention describes a novel method for determining (M1) the content
CC   of active parathyroid hormone (A) by treating a sample with (i) antibody
CC   (Ab1) that recognizes the epitope formed by amino acids (aa) 1-3 of (A),
CC   and including the N-terminal residue and (ii) antibody (Ab2) that
CC   recognizes an epitope within the receptor-binding site of (A). The number
CC   of molecules that react with both antibodies is determined and used to
CC   calculate the content of physiologically active (A). The method is used
CC   for diagnosis of calcium-metabolism disorders, osteopathy, or hypo- or
CC   hyper-parathyroidism. The method (unlike known assays) recognizes that
CC   (i) some fragments of (A) shorter than the complete (84 aa) peptide are
CC   active and (ii) that apparently intact peptide may be biologically
CC   inactive, and also takes into account the fact that some fragments of (A)
CC   are antagonistic (these have the receptor-binding site but lack the N-
CC   terminus). It thus provides a true measure of the content of
CC   physiologically active (A); contrast methods that measure intact peptide
CC   and its 1-37 fragment which may produce falsely high values. This
CC   sequence represents a peptide fragment used to illustrate the method of
CC   the invention
XX
SQ   Sequence 10 AA;

  Query Match             68.9%;  Score 42;  DB 4;  Length 10;
  Best Local Similarity   80.0%;  Pred. No. 0.37;
  Matches    8;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 AVSEIQFMHN 10
              :|||||  |||
Db          1 SVSEIQLMHN 10


RESULT 7
ABR44166
ID   ABR44166 standard; peptide; 10 AA.
XX
AC   ABR44166;
XX
DT   04-AUG-2003  (first entry)
XX
DE   Human parathyroid hormone (hPTH) fragment (residues 1-10).
XX
KW   Fusion peptide; tat; hPTHDP; parathyroid hormone; skin; cosmetic;
KW   lipolysis; human; hPTH.
XX
OS   Homo sapiens.
XX
PN   WO2003035697-A1.
XX
PD   01-MAY-2003.
XX
PF   06-MAY-2002; 2002WO-KR000835.
XX
PR   27-SEP-2001; 2001KR-00060245.
PR   15-MAR-2002; 2002KR-00014062.
XX
PA   (GLDS ) LG HOUSEHOLD & HEALTH CARE LTD.
XX
PI   Song Y,  Kang N,  Park S,  Cho W,  Kang S,  Lee Y,  Lim J,  Min H;
PI   Chang M;
XX
DR   WPI; 2003-468288/44.
XX
PT   Novel fusion peptide comprising self cell-penetrating Tat peptide bound
PT   to human parathyroid hormone-derived peptide, useful as component of skin
PT   slimming cosmetic composition.
XX
PS   Claim 5; Page 6; 32pp; English.
XX
CC   The invention relates to a fusion peptide (Tat-hPTHDP), where self cell-
CC   penetrating Tat peptide is bound to human parathyroid hormone-derived
CC   peptide (hPTHDP). The fusion peptide is useful as a component of skin
CC   slimming cosmetic composition. The fusion peptide does not cause
CC   irritation, easily and safely penetrates into integument and endothelium,
CC   does not cause skin disease and has superior lipolysis effects, and is
CC   durable. The present sequence represents a human parathyroid hormone
CC   (hPTH) fragment that can be used to construct the fusion peptide
XX
SQ   Sequence 10 AA;

  Query Match             68.9%;  Score 42;  DB 6;  Length 10;
  Best Local Similarity   80.0%;  Pred. No. 0.37;
  Matches    8;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 AVSEIQFMHN 10
              :|||||  |||
Db          1 SVSEIQLMHN 10


RESULT 8
AAY50600
ID   AAY50600 standard; peptide; 11 AA.
XX
AC   AAY50600;
XX
DT   09-FEB-2000  (first entry)
XX
DE   Resin bound cyclic peptide 33.
XX
KW   Cyclic peptide; resin bound; parathyroid hormone; osteopathic; disease;
KW   hypotensive; PTH receptor; treatment; hyper-calcemia; hypo-calcemia;
KW   osteoporosis; osteopenia; hyper-parathyroidism; hypo-parathyroidism;
KW   Cushing's syndrome; renal failure; hypertension; bone fracture repair.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 1
FT                   /note= "FMOC-Ala"
FT   Misc-difference 3
FT                   /note= "Ser(OtBu)"
```

```
FT   Misc-difference 4
FT                   /note= "Glu(OtBu)"
FT   Misc-difference 6
FT                   /note= "Gln(Trt)"
FT   Misc-difference 9
FT                   /note= "His(Trt)"
FT   Misc-difference 10
FT                   /note= "Asn(Trt)"
XX
PN   WO9952933-A1.
XX
PD   21-OCT-1999.
XX
PF   15-APR-1999;   99WO-US008435.
XX
PR   15-APR-1998;   98US-0081897P.
XX
PA   (RHON ) RHONE-POULENC RORER PHARM INC.
XX
PI   Sledeski AW,  Mencel JJ;
XX
DR   WPI; 1999-633822/54.
XX
PT   Convergent synthesis of peptides for treating e.g. bone disorders.
XX
PS   Disclosure; Page 75; 85pp; English.
XX
CC   This invention describes a novel method for the preparation of peptides
CC   (II) that contain both cyclic and linear peptide fragments comprises
CC   sequential reaction of a resin-bound linear fragment with the cyclic
CC   fragment in N-protected form and optionally other linear fragments. The
CC   products of the invention have osteopathic and hypotensive activity. (II)
CC   bind to hPTH receptors and act as agonists or antagonists of hPTH. The
CC   method is particularly used to prepare cyclic peptide analogs of
CC   parathyroid hormone (PTH) or PTH-related peptides which are useful for
CC   treating diseases that respond to treatment with agents that bind to PTH
CC   receptors (with or without activation of adenylyl cyclase activity), e.g.
CC   hyper- or hypo-calcemia, osteoporosis, osteopenia, hyper- or hypo-
CC   parathyroidism, Cushing's syndrome, renal failure and hypertension, also
CC   for promoting repair of bone fractures. Separate synthesis of the cyclic
CC   fragment allows convergent synthesis of resin-bound (II), with better
CC   yields and higher throughput. The difficulties associated with
CC   preparation of the bridged fragment are confined to a small peptide which
CC   can be purified before reaction with the resin-bound component. AAY50568-
CC   Y50614 represent the peptide fragments described in the method of the
CC   invention
XX
SQ   Sequence 11 AA;

  Query Match             68.0%;  Score 41.5;  DB 2;  Length 11;
  Best Local Similarity   83.3%;  Pred. No. 0.5;
  Matches   10;  Conservative    1;  Mismatches    0;  Indels    1;  Gaps    1;

Qy          1 AVSEIQFMHNLG 12
              |||||| :||||
Db          1 AVSEIQ-LHNLG 11


RESULT 9
AAB86225
ID   AAB86225 standard; peptide; 9 AA.
XX
AC   AAB86225;
XX
DT   03-SEP-2001  (first entry)
XX
DE   Human parathyroid hormone immunogenic peptide SEQ ID 7.
XX
KW   Parathyroid hormone; hPTH; immunogenic peptide; human; epitope;
KW   diagnosis; calcium-metabolism disorder; osteopathy; antagonist;
KW   hypo-parathyroidism; hyper-parathyroidism.
XX
OS   Homo sapiens.
XX
PN   DE19961350-A1.
XX
PD   21-JUN-2001.
XX
PF   17-DEC-1999;   99DE-01061350.
XX
PR   17-DEC-1999;   99DE-01061350.
XX
PA   (IMMU-) IMMUNDIAGNOSTIK AG.
XX
PI   Armbruster FP;
XX
DR   WPI; 2001-376318/40.
XX
PT   Determining the content of physiologically active parathyroid hormone,
PT   useful in diagnosis of calcium-metabolism disorders, using two antibodies
PT   reactive with different epitopes.
XX
PS   Disclosure; Page 3; 10pp; German.
XX
CC   This invention describes a novel method for determining (M1) the content
CC   of active parathyroid hormone (A) by treating a sample with (i) antibody
CC   (Ab1) that recognizes the epitope formed by amino acids (aa) 1-3 of (A),
CC   and including the N-terminal residue and (ii) antibody (Ab2) that
CC   recognizes an epitope within the receptor-binding site of (A). The number
CC   of molecules that react with both antibodies is determined and used to
CC   calculate the content of physiologically active (A). The method is used
CC   for diagnosis of calcium-metabolism disorders, osteopathy, or hypo- or
CC   hyper-parathyroidism. The method (unlike known assays) recognizes that
CC   (i) some fragments of (A) shorter than the complete (84 aa) peptide are
CC   active and (ii) that apparently intact peptide may be biologically
CC   inactive, and also takes into account the fact that some fragments of (A)
CC   are antagonistic (these have the receptor-binding site but lack the N-
CC   terminus). It thus provides a true measure of the content of
CC   physiologically active (A); contrast methods that measure intact peptide
CC   and its 1-37 fragment which may produce falsely high values. This
CC   sequence represents a peptide fragment used to illustrate the method of
CC   the invention
XX
SQ   Sequence 9 AA;

  Query Match             67.2%;  Score 41;  DB 4;  Length 9;
  Best Local Similarity   88.9%;  Pred. No. 1.4e+06;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 VSEIQFMHN 10
              ||||| |||
Db          1 VSEIQLMHN 9


RESULT 10
AAB01862
ID   AAB01862 standard; peptide; 9 AA.
XX
AC   AAB01862;
XX
DT   11-SEP-2000  (first entry)
XX
DE   PTH(1-14)/PTHrP(1-14)-derived peptide, SEQ ID NO:6.
XX
KW   Parathyroid hormone peptide; PTH; PTH-related peptide; PTHrP;
KW   calcium homeostasis; PTH-1 receptor; PTH-2; vitamin D synthesis;
KW   bone synthesis; agonist; osteoporosis; non-parenteral delivery.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200023594-A1.
XX
PD   27-APR-2000.
XX
PF   20-OCT-1999;   99WO-US024481.
```

XX
PR 22-OCT-1998; 98US-0105530P.
XX
PA (GARD/) GARDELLA T J.
PA (KRON/) KRONENBERG H M.
PA (POTT/) POTTS J T.
PA (JUEP/) JUEPPNER H.
XX
PI Gardella TJ, Kronenberg HM, Potts JT, Jueppner H;
XX
DR WPI; 2000-339693/29.
XX
PT Parathyroid hormone (PTH) peptides, PTH related peptides and the nucleic
PT acids that encode them, useful for treating osteoporosis.
XX
PS Disclosure; Page 26; 73pp; English.
XX
CC The invention relates to a novel parathyroid hormone (PTH) peptide
CC (AAB01859) and parathyroid hormone-related peptide (PTHrP; AAB01860), and
CC biologically active derivatives thereof (AAB01857-B01858, AAB01861-
CC B01869). The peptides of the invention are at least 85% identical to the
CC generic peptide of the formula: X1-Val-Ser-Glu-X2-Gln-Leu-X3-His-X4-X5-
CC Gly-Lys-X6 (AAB01857) where: X1 is Ser or Ala; X2 is Ile or Lys; X3 is
CC Met, Leu or Nle; X4 is Asn or Asp; X5 is Leu or Lys; X6 is His or Ser;
CC provided that the peptide is not PTHrP(1-14). The peptides of the
CC invention also encompass fragments of peptides of the invention
CC consisting of amino acids 1-9, 1-10, 1-11, 1-12 and 1-13, and N- and C-
CC terminal derivatives. PTH is a major regulator of calcium homeostasis,
CC and is necessary for the normal function of the gastrointestinal,
CC skeletal, neurological system, neuromuscular and cardiovascular systems.
CC It binds to both PTH-1 receptors on osteoblasts and renal tubular cells,
CC and to the recently identified PTH-2 receptor. PTH has a potent anabolic
CC effect on the skeleton, and mediates calcium reabsorption, enhances
CC phosphate clearance and vitamin D synthesis in the kidney. A homologous
CC calls of protein hormones, the PTH-related proteins (PTHrP) mimic some of
CC the renal and skeletal actions of PTH, and also bind to the PTH-1
CC receptor. They do not bind to the PTH-2 receptor. The peptides of the
CC invention are either agonists of PTH-1 and PTH-2 receptors (AAB01858,
CC AAB01861-B01866) or are PTH-1/PTH-2 receptor antagonists (AAB01867-
CC B01869). PTH-1/PTH-2 receptor agonists are useful for the treatment of
CC conditions characterised by a decrease in bone mass, such as
CC osteoporosis. PTH-1/PTH-2 receptor antagonists are useful for treating
CC medical disorders that arise from excessive or altered action of the PTH-
CC 1/PTH-2 receptor. Detectably labelled peptides of the invention are also
CC useful in the determination of rates of bone formation, bone resorption
CC and/or bone remodelling in a patient. The peptides of the invention are
CC "minimised" versions of PTH or PTHrP which are inexpensive to prepare by
CC conventional synthetic chemistry, and can be delivered to a patient via
CC non-parenteral routes. Sequences AAB01858 and AAB01861-B01866 represent
CC PTH-1/PTH-2 receptor agonists
XX
SQ Sequence 9 AA;

Query Match 63.9%; Score 39; DB 3; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.4e+06;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AVSEIQFMH 9
|||||| ||
Db 1 AVSEIQLMH 9

RESULT 11
AAY96966
ID AAY96966 standard; peptide; 9 AA.
XX
AC AAY96966;
XX
DT 31-OCT-2000 (first entry)
XX
DE Parathyroid hormone N-terminal signaling domain (residues 1-9).
XX
KW PTH; parathyroid hormone; N-terminal; signaling domain; bone mass;
KW bone reformation; resorption; remodeling; tether1; osteoporosis.
XX
OS Homo sapiens.
XX
PN WO200039278-A2.
XX
PD 06-JUL-2000.
XX
PF 30-DEC-1999; 99WO-US031108.
XX
PR 31-DEC-1998; 98US-0114577P.
XX
PA (GARD/) GARDELLA T J.
PA (KRON/) KRONENBERG H M.
PA (POTT/) POTTS J T.
PA (JUEP/) JUEPPNER H.
XX
PI Gardella TJ, Kronenberg HM, Potts JT, Jueppner H;
XX
DR WPI; 2000-452384/39.
XX
PT New compound comprising an amino terminal signaling functional domain
PT linked to a carboxy-terminal binding portion of parathyroid hormone for
PT treating mammalian conditions characterized by decreases in bone mass.
XX
PS Claim 4; Page 92; 119pp; English.
XX
CC Compounds of the structure or formula S-(L)_n-B, R_1-S-(L)_n-R or S-(L)_n
CC -R, are new. S is an amino terminal signaling functional domain of
CC parathyroid hormone (PTH); L is a linker molecule present n times (where
CC n is a positive integer 1-10 (preferably 4)); B is a C-terminal binding
CC portion of PTH(1-34) or a PTH-related protein (PTH-rP) (1-34); R_1 is the
CC PTH-1 receptor signal sequence; and R is (a portion of) PTH-1 receptor
CC sequence. The new compounds are used for treating mammalian conditions
CC characterized by decreases in bone mass, determining rates of bone
CC reformation, bone resorption and/or bone remodeling, treating diseases
CC and disorders associated with decreased tether1 activity, increasing cAMP
CC in a mammalian cell having PTH-1 receptors, or screening for a peptide or
CC non-peptide PTH (claimed). The new compound can be administered by
CC inhalation unlike the large native PTH or PTHrP which avoids the need for
CC regular injections to treat osteoporosis
XX
SQ Sequence 9 AA;

Query Match 63.9%; Score 39; DB 3; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.4e+06;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AVSEIQFMH 9
|||||| ||
Db 1 AVSEIQLMH 9

RESULT 12
AAR91645
ID AAR91645 standard; peptide; 9 AA.
XX
AC AAR91645;
XX
DT 06-NOV-1996 (first entry)
XX
DE Human parathyroid hormone antigenic peptide hPTH 1-9.
XX
KW Human parathyroid hormone; hPTH; antigen; alpha-helix; immunogen;
KW diagnosis; active hPTH 1-37.
XX
OS Synthetic.
XX
PN DE4434551-A1.
XX
PD 04-APR-1996.
XX
PF 28-SEP-1994; 94DE-04434551.

XX
PR 28-SEP-1994; 94DE-04434551.
XX
PA (FORS/) FORSSMANN W.
XX
PI Adermann K, Forssmann W, Hock D, Maegerlein M;
XX
DR WPI; 1996-180391/19.
XX
PT New antigenic peptide(s) from human parathyroid hormone - and antibodies
PT generated using them, able to distinguish between active and inactive
PT forms of the hormone.
XX
PS Claim 2; Page 4; 5pp; German.
XX
CC The present sequence is a specific example of claimed immunogenic
CC peptides having a sequence from hPTH(1-37) which includes the N- or C-
CC terminal alpha-helical region and/or the non-structured region of the
CC hormone. Antibodies and their binding fragments generated by injecting an
CC animal with the peptides are useful as diagnostic reagents for
CC determination of biologically active hPTH(1-37)
XX
SQ Sequence 9 AA;

Query Match 59.0%; Score 36; DB 2; Length 9;
Best Local Similarity 77.8%; Pred. No. 1.4e+06;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AVSEIQFMH 9
:||||| ||
Db 1 SVSEIQLMH 9

RESULT 13
AAB01863
ID AAB01863 standard; peptide; 9 AA.
XX
AC AAB01863;
XX
DT 11-SEP-2000 (first entry)
XX
DE PTH(1-14)/PTHrP(1-14)-derived peptide, SEQ ID NO:7.
XX
KW Parathyroid hormone peptide; PTH; PTH-related peptide; PTHrP;
KW calcium homeostasis; PTH-1 receptor; PTH-2; vitamin D synthesis;
KW bone synthesis; agonist; osteoporosis; non-parenteral delivery.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200023594-A1.
XX
PD 27-APR-2000.
XX
PF 20-OCT-1999; 99WO-US024481.
XX
PR 22-OCT-1998; 98US-0105530P.
XX
PA (GARD/) GARDELLA T J.
PA (KRON/) KRONENBERG H M.
PA (POTT/) POTTS J T.
PA (JUEP/) JUEPPNER H.
XX
PI Gardella TJ, Kronenberg HM, Potts JT, Jueppner H;
XX
DR WPI; 2000-339693/29.
XX
PT Parathyroid hormone (PTH) peptides, PTH related peptides and the nucleic
PT acids that encode them, useful for treating osteoporosis.
XX
PS Disclosure; Page 26; 73pp; English.
XX
CC The invention relates to a novel parathyroid hormone (PTH) peptide
CC (AAB01859) and parathyroid hormone-related peptide (PTHrP; AAB01860), and
CC biologically active derivatives thereof (AAB01857-B01858, AAB01861-
CC B01869). The peptides of the invention are at least 85% identical to the
CC generic peptide of the formula: X1-Val-Ser-Glu-X2-Gln-Leu-X3-His-X4-X5-
CC Gly-Lys-X6 (AAB01857) where: X1 is Ser or Ala; X2 is Ile or Lys; X3 is
CC Met, Leu or Nle; X4 is Asn or Asp; X5 is Leu or Lys; X6 is His or Ser;
CC provided that the peptide is not PTHrP(1-14). The peptides of the
CC invention also encompass fragments of peptides of the invention
CC consisting of amino acids 1-9, 1-10, 1-11, 1-12 and 1-13, and N- and C-
CC terminal derivatives. PTH is a major regulator of calcium homeostasis,
CC and is necessary for the normal function of the gastrointestinal,
CC skeletal, neurological system, neuromuscular and cardiovascular systems.
CC It binds to both PTH-1 receptors on osteoblasts and renal tubular cells,
CC and to the recently identified PTH-2 receptor. PTH has a potent anabolic
CC effect on the skeleton, and mediates calcium reabsorption, enhances
CC phosphate clearance and vitamin D synthesis in the kidney. A homologous
CC calls of protein hormones, the PTH-related proteins (PTHrP) mimic some of
CC the renal and skeletal actions of PTH, and also bind to the PTH-1
CC receptor. They do not bind to the PTH-2 receptor. The peptides of the
CC invention are either agonists of PTH-1 and PTH-2 receptors (AAB01858,
CC AAB01861-B01866) or are PTH-1/PTH-2 receptor antagonists (AAB01867-
CC B01869). PTH-1/PTH-2 receptor agonists are useful for the treatment of
CC conditions characterised by a decrease in bone mass, such as
CC osteoporosis. PTH-1/PTH-2 receptor antagonists are useful for treating
CC medical disorders that arise from excessive or altered action of the PTH-
CC 1/PTH-2 receptor. Detectably labelled peptides of the invention are also
CC useful in the determination of rates of bone formation, bone resorption
CC and/or bone remodelling in a patient. The peptides of the invention are
CC "minimised" versions of PTH or PTHrP which are inexpensive to prepare by
CC conventional synthetic chemistry, and can be delivered to a patient via
CC non-parenteral routes. Sequences AAB01858 and AAB01861-B01866 represent
CC PTH-1/PTH-2 receptor agonists
XX
SQ Sequence 9 AA;

Query Match 59.0%; Score 36; DB 3; Length 9;
Best Local Similarity 77.8%; Pred. No. 1.4e+06;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AVSEIQFMH 9
|||||| :|
Db 1 AVSEIQLLH 9

RESULT 14
AAY96981
ID AAY96981 standard; peptide; 9 AA.
XX
AC AAY96981;
XX
DT 31-OCT-2000 (first entry)
XX
DE Parathyroid hormone N-terminal signaling domain.
XX
KW PTH; parathyroid hormone; N-terminal; signaling domain; bone mass;
KW bone reformation; resorption; remodeling; tether1; osteoporosis.
XX
OS Homo sapiens.
XX
PN WO200039278-A2.
XX
PD 06-JUL-2000.
XX
PF 30-DEC-1999; 99WO-US031108.
XX
PR 31-DEC-1998; 98US-0114577P.
XX
PA (GARD/) GARDELLA T J.
PA (KRON/) KRONENBERG H M.
PA (POTT/) POTTS J T.
PA (JUEP/) JUEPPNER H.
XX
PI Gardella TJ, Kronenberg HM, Potts JT, Jueppner H;

XX
DR WPI; 2000-452384/39.
XX
PT New compound comprising an amino terminal signaling functional domain
PT linked to a carboxy-terminal binding portion of parathyroid hormone for
PT treating mammalian conditions characterized by decreases in bone mass.
XX
PS Claim 11; Page 93; 119pp; English.
XX
CC Compounds of the structure or formula S-(L)_n-B, R_1-S-(L)_n-R or S-(L)_n
CC -R, are new. S is an amino terminal signaling functional domain of
CC parathyroid hormone (PTH); L is a linker molecule present n times (where
CC n is a positive integer 1-10 (preferably 4)); B is a C-terminal binding
CC portion of PTH(1-34) or a PTH-related protein (PTH-rP) (1-34); R_1 is the
CC PTH-1 receptor signal sequence; and R is (a portion of) PTH-1 receptor
CC sequence. The new compounds are used for treating mammalian conditions
CC characterized by decreases in bone mass, determining rates of bone
CC reformation, bone resorption and/or bone remodeling, treating diseases
CC and disorders associated with decreased tether1 activity, increasing cAMP
CC in a mammalian cell having PTH-1 receptors, or screening for a peptide or
CC non-peptide PTH (claimed). The new compound can be administered by
CC inhalation unlike the large native PTH or PTHrP which avoids the need for
CC regular injections to treat osteoporosis
XX
SQ Sequence 9 AA;

Query Match 59.0%; Score 36; DB 3; Length 9;
Best Local Similarity 77.8%; Pred. No. 1.4e+06;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AVSEIQFMH 9
:||||| ||
Db 1 SVSEIQLMH 9

RESULT 15
AAB86220
ID AAB86220 standard; peptide; 9 AA.
XX
AC AAB86220;
XX
DT 03-SEP-2001 (first entry)
XX
DE Human parathyroid hormone immunogenic peptide SEQ ID 2.
XX
KW Parathyroid hormone; hPTH; immunogenic peptide; human; epitope;
KW diagnosis; calcium-metabolism disorder; osteopathy; antagonist;
KW hypo-parathyroidism; hyper-parathyroidism.
XX
OS Homo sapiens.
XX
PN DE19961350-A1.
XX
PD 21-JUN-2001.
XX
PF 17-DEC-1999; 99DE-01061350.
XX
PR 17-DEC-1999; 99DE-01061350.
XX
PA (IMMU-) IMMUNDIAGNOSTIK AG.
XX
PI Armbruster FP;
XX
DR WPI; 2001-376318/40.
XX
PT Determining the content of physiologically active parathyroid hormone,
PT useful in diagnosis of calcium-metabolism disorders, using two antibodies
PT reactive with different epitopes.
XX
PS Disclosure; Page 3; 10pp; German.
XX
CC This invention describes a novel method for determining (M1) the content
CC of active parathyroid hormone (A) by treating a sample with (i) antibody
CC (Ab1) that recognizes the epitope formed by amino acids (aa) 1-3 of (A),
CC and including the N-terminal residue and (ii) antibody (Ab2) that
CC recognizes an epitope within the receptor-binding site of (A). The number
CC of molecules that react with both antibodies is determined and used to
CC calculate the content of physiologically active (A). The method is used
CC for diagnosis of calcium-metabolism disorders, osteopathy, or hypo- or
CC hyper-parathyroidism. The method (unlike known assays) recognizes that
CC (i) some fragments of (A) shorter than the complete (84 aa) peptide are
CC active and (ii) that apparently intact peptide may be biologically
CC inactive, and also takes into account the fact that some fragments of (A)
CC are antagonistic (these have the receptor-binding site but lack the N-
CC terminus). It thus provides a true measure of the content of
CC physiologically active (A); contrast methods that measure intact peptide
CC and its 1-37 fragment which may produce falsely high values. This
CC sequence represents a peptide fragment used to illustrate the method of
CC the invention
XX
SQ Sequence 9 AA;

Query Match 59.0%; Score 36; DB 4; Length 9;
Best Local Similarity 77.8%; Pred. No. 1.4e+06;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AVSEIQFMH 9
:||||| ||
Db 1 SVSEIQLMH 9

Search completed: September 5, 2004, 09:34:31
Job time : 37.5 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: September 5, 2004, 09:37:09 ; Search time 32.5 Seconds
(without alignments)
116.332 Million cell updates/sec

Title: US-09-730-174A-6
Perfect score: 61
Sequence: 1 AVSEIQFMHNLG 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1298764 seqs, 315065143 residues

Total number of hits satisfying chosen parameters: 182187

Minimum DB seq length: 0
Maximum DB seq length: 12

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	61	100.0	12	9	US-09-730-174A-6	Sequence 6, Appli
2	58	95.1	12	9	US-09-730-174A-4	Sequence 4, Appli
3	57	93.4	11	9	US-09-730-174A-2	Sequence 2, Appli
4	55	90.2	12	9	US-09-730-174A-5	Sequence 5, Appli
5	52	85.2	12	9	US-09-730-174A-3	Sequence 3, Appli
6	51	83.6	11	9	US-09-730-174A-1	Sequence 1, Appli
7	42	68.9	10	14	US-10-168-185-1	Sequence 1, Appli
8	41	67.2	9	14	US-10-168-185-7	Sequence 7, Appli
9	39	63.9	9	14	US-10-192-673-6	Sequence 6, Appli
10	37	60.7	8	14	US-10-168-185-8	Sequence 8, Appli
11	36	59.0	9	14	US-10-192-673-7	Sequence 7, Appli
12	36	59.0	9	14	US-10-168-185-2	Sequence 2, Appli
13	29	47.5	9	14	US-10-192-673-8	Sequence 8, Appli
14	28	45.9	8	14	US-10-168-185-3	Sequence 3, Appli
15	27	44.3	10	14	US-10-232-187-8	Sequence 8, Appli
16	27	44.3	10	15	US-10-366-709-2	Sequence 2, Appli
17	26	42.6	9	14	US-10-192-673-10	Sequence 10, Appl
18	25	41.0	10	9	US-09-976-787-4	Sequence 4, Appli
19	25	41.0	10	9	US-09-865-198-4	Sequence 4, Appli
20	25	41.0	10	9	US-09-965-099-12	Sequence 12, Appl
21	25	41.0	10	10	US-09-563-222-41	Sequence 41, Appl
22	25	41.0	10	10	US-09-798-689-4	Sequence 4, Appli
23	25	41.0	10	12	US-10-239-656-19	Sequence 19, Appl
24	25	41.0	10	13	US-10-051-852-12	Sequence 12, Appl
25	25	41.0	10	14	US-10-195-752-108	Sequence 108, App
26	25	41.0	10	14	US-10-160-232-12	Sequence 12, Appl
27	25	41.0	10	14	US-10-160-232-18	Sequence 18, Appl
28	25	41.0	10	14	US-10-283-349-49	Sequence 49, Appl
29	25	41.0	10	14	US-10-230-880-115	Sequence 115, App
30	25	41.0	10	15	US-10-137-867-526	Sequence 526, App
31	25	41.0	10	15	US-10-366-709-3	Sequence 3, Appli
32	25	41.0	10	15	US-10-430-176-12	Sequence 12, Appl
33	25	41.0	11	11	US-09-791-551-13	Sequence 13, Appl
34	24	39.3	9	9	US-09-834-765-45	Sequence 45, Appl
35	24	39.3	9	9	US-09-834-765-55	Sequence 55, Appl
36	24	39.3	10	9	US-09-834-765-73	Sequence 73, Appl
37	24	39.3	10	9	US-09-834-765-78	Sequence 78, Appl
38	24	39.3	10	9	US-09-910-059-26	Sequence 26, Appl
39	24	39.3	10	14	US-10-033-741-61	Sequence 61, Appl
40	24	39.3	11	14	US-10-153-334-14	Sequence 14, Appl
41	24	39.3	11	16	US-10-391-364-93	Sequence 93, Appl
42	24	39.3	12	14	US-10-319-130-16	Sequence 16, Appl
43	23	37.7	6	14	US-10-168-185-5	Sequence 5, Appli
44	23	37.7	7	14	US-10-168-185-4	Sequence 4, Appli
45	23	37.7	8	14	US-10-043-487-508	Sequence 508, App

ALIGNMENTS

RESULT 1
US-09-730-174A-6
; Sequence 6, Application US/09730174A
; Patent No. US20020110871A1
; GENERAL INFORMATION:
; APPLICANT: Zahradnik, R.J.
; TITLE OF INVENTION: Antibodies and Peptide Antigens for Producing Antibodies having
; TITLE OF INVENTION: Selective Binding Specificity to Bioactive Intact Parathyroid H
; FILE REFERENCE: IMUNE-001A
; CURRENT APPLICATION NUMBER: US/09/730,174A
; CURRENT FILING DATE: 2000-12-05
; NUMBER OF SEQ ID NOS: 12
; SEQ ID NO 6
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Induces Formation of Antibodies and Isolates said Antibodies
US-09-730-174A-6

Query Match 100.0%; Score 61; DB 9; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.00014;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 AVSEIQFMHNLG 12
              ||||||||||||
Db          1 AVSEIQFMHNLG 12
```

RESULT 2
US-09-730-174A-4
; Sequence 4, Application US/09730174A
; Patent No. US20020110871A1
; GENERAL INFORMATION:
; APPLICANT: Zahradnik, R.J.
; TITLE OF INVENTION: Antibodies and Peptide Antigens for Producing Antibodies having
; TITLE OF INVENTION: Selective Binding Specificity to Bioactive Intact Parathyroid H
; FILE REFERENCE: IMUNE-001A

```
;  CURRENT APPLICATION NUMBER: US/09/730,174A
;  CURRENT FILING DATE:  2000-12-05
;  NUMBER OF SEQ ID NOS: 12
; SEQ ID NO 4
;   LENGTH: 12
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Induces Formation of Antibodies and Isolates said Antibodies
US-09-730-174A-4

  Query Match             95.1%;  Score 58;  DB 9;  Length 12;
  Best Local Similarity   91.7%;  Pred. No. 0.00049;
  Matches   11;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AVSEIQFMHNLG 12
              :||||||||||||
Db          1 SVSEIQFMHNLG 12


RESULT 3
US-09-730-174A-2
; Sequence 2, Application US/09730174A
; Patent No. US20020110871A1
; GENERAL INFORMATION:
;  APPLICANT: Zahradnik, R.J.
;  TITLE OF INVENTION: Antibodies and Peptide Antigens for Producing Antibodies having a
;  TITLE OF INVENTION:  Selective Binding Specificity to Bioactive Intact Parathyroid Ho
;  FILE REFERENCE: IMUNE-001A
;  CURRENT APPLICATION NUMBER: US/09/730,174A
;  CURRENT FILING DATE:  2000-12-05
;  NUMBER OF SEQ ID NOS: 12
; SEQ ID NO 2
;   LENGTH: 11
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Induces Formation of Antibodies and Isolates said Antibodies
US-09-730-174A-2

  Query Match             93.4%;  Score 57;  DB 9;  Length 11;
  Best Local Similarity   100.0%;  Pred. No. 0.00068;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 VSEIQFMHNLG 12
              ||||||||||||
Db          1 VSEIQFMHNLG 11


RESULT 4
US-09-730-174A-5
; Sequence 5, Application US/09730174A
; Patent No. US20020110871A1
; GENERAL INFORMATION:
;  APPLICANT: Zahradnik, R.J.
;  TITLE OF INVENTION: Antibodies and Peptide Antigens for Producing Antibodies having a
;  TITLE OF INVENTION:  Selective Binding Specificity to Bioactive Intact Parathyroid Ho
;  FILE REFERENCE: IMUNE-001A
;  CURRENT APPLICATION NUMBER: US/09/730,174A
;  CURRENT FILING DATE:  2000-12-05
;  NUMBER OF SEQ ID NOS: 12
; SEQ ID NO 5
;   LENGTH: 12
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Induces Formation of Antibodies and Isolates said Antibodies
US-09-730-174A-5

  Query Match             90.2%;  Score 55;  DB 9;  Length 12;
  Best Local Similarity   91.7%;  Pred. No. 0.0018;
  Matches   11;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 AVSEIQFMHNLG 12
              ||||||.|||||
Db          1 AVSEIQLMHNLG 12


RESULT 5
US-09-730-174A-3
; Sequence 3, Application US/09730174A
; Patent No. US20020110871A1
; GENERAL INFORMATION:
;  APPLICANT: Zahradnik, R.J.
;  TITLE OF INVENTION: Antibodies and Peptide Antigens for Producing Antibodies having a
;  TITLE OF INVENTION:  Selective Binding Specificity to Bioactive Intact Parathyroid Ho
;  FILE REFERENCE: IMUNE-001A
;  CURRENT APPLICATION NUMBER: US/09/730,174A
;  CURRENT FILING DATE:  2000-12-05
;  NUMBER OF SEQ ID NOS: 12
; SEQ ID NO 3
;   LENGTH: 12
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Induces Formation of Antibodies and Isolates said Antibodies
US-09-730-174A-3

  Query Match             85.2%;  Score 52;  DB 9;  Length 12;
  Best Local Similarity   83.3%;  Pred. No. 0.0063;
  Matches   10;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 AVSEIQFMHNLG 12
              :|||||.|||||
Db          1 SVSEIQLMHNLG 12


RESULT 6
US-09-730-174A-1
; Sequence 1, Application US/09730174A
; Patent No. US20020110871A1
; GENERAL INFORMATION:
;  APPLICANT: Zahradnik, R.J.
;  TITLE OF INVENTION: Antibodies and Peptide Antigens for Producing Antibodies having a
;  TITLE OF INVENTION:  Selective Binding Specificity to Bioactive Intact Parathyroid Ho
;  FILE REFERENCE: IMUNE-001A
;  CURRENT APPLICATION NUMBER: US/09/730,174A
;  CURRENT FILING DATE:  2000-12-05
;  NUMBER OF SEQ ID NOS: 12
; SEQ ID NO 1
;   LENGTH: 11
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Induces Formation of Antibodies and Isolates said Antibodies
US-09-730-174A-1

  Query Match             83.6%;  Score 51;  DB 9;  Length 11;
  Best Local Similarity   90.9%;  Pred. No. 0.0089;
  Matches   10;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 VSEIQFMHNLG 12
              |||||.|||||
Db          1 VSEIQLMHNLG 11


RESULT 7
US-10-168-185-1
; Sequence 1, Application US/10168185
; Publication No. US20030175802A1
; GENERAL INFORMATION:
;  APPLICANT: Armbruster, Franz Paul
;  APPLICANT:  Missbichler, Albert
;  APPLICANT:  Schmidt-Gayk, Heinrich
;  APPLICANT:  Roth, Heinz-Jurgen
;  TITLE OF INVENTION: Method for Determining Parathormone
```

```
;  TITLE OF INVENTION:  Activity in a Human Sample
;  FILE REFERENCE: HLZ-004US
;  CURRENT APPLICATION NUMBER: US/10/168,185
;  CURRENT FILING DATE:  2002-06-17
;  PRIOR APPLICATION NUMBER: PCT/EP00/12911
;  PRIOR FILING DATE: 2000-12-18
;  PRIOR APPLICATION NUMBER: DE 19961350
;  PRIOR FILING DATE: 1999-12-17
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 10
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-168-185-1

  Query Match             68.9%;  Score 42;  DB 14;  Length 10;
  Best Local Similarity   80.0%;  Pred. No. 0.38;
  Matches    8;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 AVSEIQFMHN 10
              :|||||  |||
Db          1 SVSEIQLMHN 10


RESULT 8
US-10-168-185-7
; Sequence 7, Application US/10168185
; Publication No. US20030175802A1
; GENERAL INFORMATION:
;  APPLICANT: Armbruster, Franz Paul
;  APPLICANT:  Missbichler, Albert
;  APPLICANT:  Schmidt-Gayk, Heinrich
;  APPLICANT:  Roth, Heinz-Jurgen
;  TITLE OF INVENTION: Method for Determining Parathormone
;  TITLE OF INVENTION:  Activity in a Human Sample
;  FILE REFERENCE: HLZ-004US
;  CURRENT APPLICATION NUMBER: US/10/168,185
;  CURRENT FILING DATE:  2002-06-17
;  PRIOR APPLICATION NUMBER: PCT/EP00/12911
;  PRIOR FILING DATE: 2000-12-18
;  PRIOR APPLICATION NUMBER: DE 19961350
;  PRIOR FILING DATE: 1999-12-17
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-168-185-7

  Query Match             67.2%;  Score 41;  DB 14;  Length 9;
  Best Local Similarity   88.9%;  Pred. No. 1.2e+06;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 VSEIQFMHN 10
              |||||  |||
Db          1 VSEIQLMHN 9


RESULT 9
US-10-192-673-6
; Sequence 6, Application US/10192673
; Publication No. US20030166838A1
; GENERAL INFORMATION:
;  APPLICANT: Gardella, Thomas J.
;  APPLICANT:  Kronenberg, Henry
;  APPLICANT:  Potts, John T.
;  APPLICANT:  Juppner, Harald
;  TITLE OF INVENTION: Bioactive Peptides and Peptide Derivatives of
;  TITLE OF INVENTION:  Parathyroid Hormone (PTH) and Parathyroid
;  TITLE OF INVENTION:  Hormone-Related Peptide (PTHrP)
;  FILE REFERENCE: 0609.4570002
;  CURRENT APPLICATION NUMBER: US/10/192,673
;  CURRENT FILING DATE:  2002-07-11
;  PRIOR APPLICATION NUMBER: U.S. 09/421,379
;  PRIOR FILING DATE: 1999-10-20
;  PRIOR APPLICATION NUMBER: U.S. 60/105,530
;  PRIOR FILING DATE: 1998-10-22
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: synthetic
;   OTHER INFORMATION: peptide
US-10-192-673-6

  Query Match             63.9%;  Score 39;  DB 14;  Length 9;
  Best Local Similarity   88.9%;  Pred. No. 1.2e+06;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 AVSEIQFMH 9
              ||||||  ||
Db          1 AVSEIQLMH 9


RESULT 10
US-10-168-185-8
; Sequence 8, Application US/10168185
; Publication No. US20030175802A1
; GENERAL INFORMATION:
;  APPLICANT: Armbruster, Franz Paul
;  APPLICANT:  Missbichler, Albert
;  APPLICANT:  Schmidt-Gayk, Heinrich
;  APPLICANT:  Roth, Heinz-Jurgen
;  TITLE OF INVENTION: Method for Determining Parathormone
;  TITLE OF INVENTION:  Activity in a Human Sample
;  FILE REFERENCE: HLZ-004US
;  CURRENT APPLICATION NUMBER: US/10/168,185
;  CURRENT FILING DATE:  2002-06-17
;  PRIOR APPLICATION NUMBER: PCT/EP00/12911
;  PRIOR FILING DATE: 2000-12-18
;  PRIOR APPLICATION NUMBER: DE 19961350
;  PRIOR FILING DATE: 1999-12-17
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
;   LENGTH: 8
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-168-185-8

  Query Match             60.7%;  Score 37;  DB 14;  Length 8;
  Best Local Similarity   87.5%;  Pred. No. 1.2e+06;
  Matches    7;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 SEIQFMHN 10
              ||||  |||
Db          1 SEIQLMHN 8


RESULT 11
US-10-192-673-7
; Sequence 7, Application US/10192673
; Publication No. US20030166838A1
; GENERAL INFORMATION:
;  APPLICANT: Gardella, Thomas J.
;  APPLICANT:  Kronenberg, Henry
;  APPLICANT:  Potts, John T.
;  APPLICANT:  Juppner, Harald
;  TITLE OF INVENTION: Bioactive Peptides and Peptide Derivatives of
;  TITLE OF INVENTION:  Parathyroid Hormone (PTH) and Parathyroid
;  TITLE OF INVENTION:  Hormone-Related Peptide (PTHrP)
```

```
;  FILE REFERENCE: 0609.4570002
;  CURRENT APPLICATION NUMBER: US/10/192,673
;  CURRENT FILING DATE:  2002-07-11
;  PRIOR APPLICATION NUMBER: U.S. 09/421,379
;  PRIOR FILING DATE: 1999-10-20
;  PRIOR APPLICATION NUMBER: U.S. 60/105,530
;  PRIOR FILING DATE: 1998-10-22
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: synthetic
;   OTHER INFORMATION: peptide
US-10-192-673-7

  Query Match             59.0%;  Score 36;  DB 14;  Length 9;
  Best Local Similarity   77.8%;  Pred. No. 1.2e+06;
  Matches    7;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 AVSEIQFMH 9
              |||||| :|
Db          1 AVSEIQLLH 9


RESULT 12
US-10-168-185-2
; Sequence 2, Application US/10168185
; Publication No. US20030175802A1
; GENERAL INFORMATION:
;  APPLICANT: Armbruster, Franz Paul
;  APPLICANT:  Missbichler, Albert
;  APPLICANT:  Schmidt-Gayk, Heinrich
;  APPLICANT:  Roth, Heinz-Jurgen
;  TITLE OF INVENTION: Method for Determining Parathormone
;  TITLE OF INVENTION:  Activity in a Human Sample
;  FILE REFERENCE: HLZ-004US
;  CURRENT APPLICATION NUMBER: US/10/168,185
;  CURRENT FILING DATE:  2002-06-17
;  PRIOR APPLICATION NUMBER: PCT/EP00/12911
;  PRIOR FILING DATE: 2000-12-18
;  PRIOR APPLICATION NUMBER: DE 19961350
;  PRIOR FILING DATE: 1999-12-17
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-168-185-2

  Query Match             59.0%;  Score 36;  DB 14;  Length 9;
  Best Local Similarity   77.8%;  Pred. No. 1.2e+06;
  Matches    7;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 AVSEIQFMH 9
              :||||| ||
Db          1 SVSEIQLMH 9


RESULT 13
US-10-192-673-8
; Sequence 8, Application US/10192673
; Publication No. US20030166838A1
; GENERAL INFORMATION:
;  APPLICANT: Gardella, Thomas J.
;  APPLICANT:  Kronenberg, Henry
;  APPLICANT:  Potts, John T.
;  APPLICANT:  Juppner, Harald
;  TITLE OF INVENTION: Bioactive Peptides and Peptide Derivatives of
;  TITLE OF INVENTION:  Parathyroid Hormone (PTH) and Parathyroid
;  TITLE OF INVENTION:  Hormone-Related Peptide (PTHrP)
;  FILE REFERENCE: 0609.4570002
;  CURRENT APPLICATION NUMBER: US/10/192,673
;  CURRENT FILING DATE:  2002-07-11
;  PRIOR APPLICATION NUMBER: U.S. 09/421,379
;  PRIOR FILING DATE: 1999-10-20
;  PRIOR APPLICATION NUMBER: U.S. 60/105,530
;  PRIOR FILING DATE: 1998-10-22
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: synthetic
;   OTHER INFORMATION: peptide
US-10-192-673-8

  Query Match             47.5%;  Score 29;  DB 14;  Length 9;
  Best Local Similarity   66.7%;  Pred. No. 1.2e+06;
  Matches    6;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 AVSEIQFMH 9
              |||| | :|
Db          1 AVSEHQLLH 9


RESULT 14
US-10-168-185-3
; Sequence 3, Application US/10168185
; Publication No. US20030175802A1
; GENERAL INFORMATION:
;  APPLICANT: Armbruster, Franz Paul
;  APPLICANT:  Missbichler, Albert
;  APPLICANT:  Schmidt-Gayk, Heinrich
;  APPLICANT:  Roth, Heinz-Jurgen
;  TITLE OF INVENTION: Method for Determining Parathormone
;  TITLE OF INVENTION:  Activity in a Human Sample
;  FILE REFERENCE: HLZ-004US
;  CURRENT APPLICATION NUMBER: US/10/168,185
;  CURRENT FILING DATE:  2002-06-17
;  PRIOR APPLICATION NUMBER: PCT/EP00/12911
;  PRIOR FILING DATE: 2000-12-18
;  PRIOR APPLICATION NUMBER: DE 19961350
;  PRIOR FILING DATE: 1999-12-17
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
;   LENGTH: 8
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-168-185-3

  Query Match             45.9%;  Score 28;  DB 14;  Length 8;
  Best Local Similarity   75.0%;  Pred. No. 1.2e+06;
  Matches    6;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 AVSEIQFM 8
              :||||| |
Db          1 SVSEIQLM 8


RESULT 15
US-10-232-187-8
; Sequence 8, Application US/10232187
; Publication No. US20030092091A1
; GENERAL INFORMATION:
;  APPLICANT: Abrahamson, Julie A.
;  APPLICANT:  Bochner, Bruce
;  APPLICANT:  Erickson-Miller, Connie L.
;  APPLICANT:  Kikly, Kristine K.
;  APPLICANT:  Schleimer, Robert
```

```
;  APPLICANT:  Nulku, Turkan E.
;  TITLE OF INVENTION: Sialoadhesin Factor-2 Antibodies
;  FILE REFERENCE: GH50042-1
;  CURRENT APPLICATION NUMBER: US/10/232,187
;  CURRENT FILING DATE:  2002-08-29
;  PRIOR APPLICATION NUMBER: 60/187,595
;  PRIOR FILING DATE: 2000-03-07
;  PRIOR APPLICATION NUMBER: PCT/US01/07193
;  PRIOR FILING DATE: 2001-03-05
;  PRIOR APPLICATION NUMBER: 60/315,943
;  PRIOR FILING DATE: 2001-08-30
;  PRIOR APPLICATION NUMBER: 60/349,830
;  PRIOR FILING DATE: 2002-01-18
;  PRIOR APPLICATION NUMBER: 60/394,741
;  PRIOR FILING DATE: 2002-07-10
;  NUMBER OF SEQ ID NOS: 14
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
;   LENGTH: 10
;   TYPE: PRT
;   ORGANISM: Homo sapien
US-10-232-187-8

  Query Match            44.3%;  Score 27;  DB 14;  Length 10;
  Best Local Similarity  44.4%;  Pred. No. 2.3e+02;
  Matches    4;  Conservative    2;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 AVSEIQFMH 9
              | |  : :||
Db          2 ATSSVSYMH 10


Search completed: September  5, 2004, 09:49:38
Job time : 32.5 secs
```

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: September 5, 2004, 09:32:03 ; Search time 11 Seconds
(without alignments)
56.319 Million cell updates/sec

Title: US-09-730-174A-6
Perfect score: 61
Sequence: 1 AVSEIQFMHNLG 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 121490

Minimum DB seq length: 0
Maximum DB seq length: 12

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	49	80.3	12	4	US-09-442-989-31	Sequence 31, Appl
2	42	68.9	10	3	US-08-817-547A-1	Sequence 1, Appli
3	39	63.9	9	4	US-09-421-379-6	Sequence 6, Appli
4	36	59.0	9	3	US-08-817-547A-2	Sequence 2, Appli
5	36	59.0	9	4	US-09-421-379-7	Sequence 7, Appli
6	31	50.8	11	6	5460978-3	Patent No. 5460978
7	29	47.5	9	4	US-09-421-379-8	Sequence 8, Appli
8	29	47.5	12	2	US-08-140-137A-42	Sequence 42, Appl
9	28	45.9	8	3	US-08-817-547A-3	Sequence 3, Appli
10	27	44.3	12	2	US-08-482-228-42	Sequence 42, Appl
11	27	44.3	12	3	US-08-482-528-42	Sequence 42, Appl
12	26	42.6	9	4	US-09-421-379-10	Sequence 10, Appl
13	25	41.0	10	2	US-08-116-778E-9	Sequence 9, Appli
14	25	41.0	10	2	US-08-438-562-9	Sequence 9, Appli
15	25	41.0	10	2	US-08-483-528B-97	Sequence 97, Appl
16	25	41.0	10	3	US-08-783-853A-12	Sequence 12, Appl
17	25	41.0	10	3	US-08-836-561-49	Sequence 49, Appl
18	25	41.0	10	3	US-09-280-028-12	Sequence 12, Appl
19	25	41.0	10	4	US-09-344-050-12	Sequence 12, Appl
20	25	41.0	10	4	US-09-393-385B-108	Sequence 108, App
21	25	41.0	10	4	US-09-434-122-49	Sequence 49, Appl
22	25	41.0	10	4	US-09-091-071-3	Sequence 3, Appli
23	24	39.3	5	2	US-08-177-109A-56	Sequence 56, Appl
24	24	39.3	5	2	US-08-687-706-56	Sequence 56, Appl
25	24	39.3	5	3	US-08-817-547A-17	Sequence 17, Appl
26	24	39.3	6	3	US-08-817-547A-16	Sequence 16, Appl
27	24	39.3	7	3	US-08-817-547A-15	Sequence 15, Appl
28	24	39.3	8	2	US-08-748-021-64	Sequence 64, Appl
29	24	39.3	8	3	US-08-817-547A-14	Sequence 14, Appl
30	24	39.3	8	3	US-08-974-297-64	Sequence 64, Appl
31	24	39.3	9	3	US-08-817-547A-13	Sequence 13, Appl
32	24	39.3	10	1	US-08-432-694-5	Sequence 5, Appli
33	24	39.3	10	3	US-08-817-547A-7	Sequence 7, Appli
34	24	39.3	10	3	US-09-171-945-26	Sequence 26, Appl
35	24	39.3	11	1	US-08-432-694-3	Sequence 3, Appli
36	23	37.7	6	3	US-08-817-547A-5	Sequence 5, Appli
37	23	37.7	7	3	US-08-817-547A-4	Sequence 4, Appli
38	23	37.7	9	1	US-07-822-043-26	Sequence 26, Appl
39	23	37.7	9	1	US-08-346-455B-26	Sequence 26, Appl
40	23	37.7	9	3	US-08-977-221-26	Sequence 26, Appl
41	23	37.7	9	4	US-09-483-831B-26	Sequence 26, Appl
42	23	37.7	9	5	PCT-US95-06613-26	Sequence 26, Appl
43	23	37.7	10	4	US-09-771-415-3	Sequence 3, Appli
44	23	37.7	12	3	US-09-064-750-1	Sequence 1, Appli
45	22	36.1	10	1	US-08-615-181-83	Sequence 83, Appl

ALIGNMENTS

```
RESULT 1
US-09-442-989-31
; Sequence 31, Application US/09442989
; Patent No. 6569993
; GENERAL INFORMATION:
;  APPLICANT: Sledeski, Adam W.
;  APPLICANT: Mencel, James J.
;  TITLE OF INVENTION: PROCESS FOR THE PREPARATION OF RESIN-BOUND CYCLIC
;  TITLE OF INVENTION: PEPTIDES
;  FILE REFERENCE: A3113B-US
;  CURRENT APPLICATION NUMBER: US/09/442,989
;  CURRENT FILING DATE: 1999-11-18
;  EARLIER APPLICATION NUMBER: 60/081,897
;  EARLIER FILING DATE: 1998-04-15
;  NUMBER OF SEQ ID NOS: 46
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 31
;   LENGTH: 12
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: PEPTIDE
;   LOCATION: (1)
;   OTHER INFORMATION: FMOC-Ala
;   FEATURE:
;   NAME/KEY: PEPTIDE
;   LOCATION: (3)
;   OTHER INFORMATION: Ser(OtBu)
;   FEATURE:
;   NAME/KEY: PEPTIDE
;   LOCATION: (4)
;   OTHER INFORMATION: Glu(OtBu)
;   FEATURE:
;   NAME/KEY: PEPTIDE
;   LOCATION: (6)
;   OTHER INFORMATION: Gln(Trt)
;   FEATURE:
;   NAME/KEY: PEPTIDE
;   LOCATION: (9)
;   OTHER INFORMATION: His(Trt)
;   FEATURE:
;   NAME/KEY: PEPTIDE
;   LOCATION: (10)
;   OTHER INFORMATION: Asn(Trt)
;   FEATURE:
;   NAME/KEY: MOD_RES
;   LOCATION: (8)
;   OTHER INFORMATION: Nle
US-09-442-989-31
```

```
  Query Match             80.3%;  Score 49;  DB 4;  Length 12;
  Best Local Similarity   83.3%;  Pred. No. 0.0034;
  Matches   10;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 AVSEIQFMHNLG 12
              ||||||  ||||
Db          1 AVSEIQLXHNLG 12


RESULT 2
US-08-817-547A-1
; Sequence 1, Application US/08817547A
; Patent No. 6030790
;  GENERAL INFORMATION:
;    APPLICANT:  Adermann, Knut
;    APPLICANT:  Hock, Dieter
;    APPLICANT:  Magerlein, Markus
;    TITLE OF INVENTION:  Peptides from the hPTH Sequence
;    NUMBER OF SEQUENCES:  36
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Jones & Askew, LLP
;      STREET:  191 Peachtree Street, 37th Floor
;      CITY:  Atlanta
;      STATE:  Georgia
;      COUNTRY:  USA
;      ZIP:  30303
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/817,547A
;      FILING DATE:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/EP95/03757
;      FILING DATE:  29 SEPT 1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  FROST, ROGER T.
;      REGISTRATION NUMBER:  22,176
;      REFERENCE/DOCKET NUMBER:  07826-0007
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  404-818-3700
;      TELEFAX:  404-818-3799
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  unknown
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  peptide
;    HYPOTHETICAL:  no
;    ANTI-SENSE:  no
US-08-817-547A-1

  Query Match             68.9%;  Score 42;  DB 3;  Length 10;
  Best Local Similarity   80.0%;  Pred. No. 0.06;
  Matches    8;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 AVSEIQFMHN 10
              :|||||  |||
Db          1 SVSEIQLMHN 10


RESULT 3
US-09-421-379-6
; Sequence 6, Application US/09421379
; Patent No. 6495662
; GENERAL INFORMATION:
;  APPLICANT: Gardella, Thomas J.
;  APPLICANT: Kronenberg, Henry
;  APPLICANT: Potts, John T.
;  APPLICANT: Juppner, Harald
;  TITLE OF INVENTION: Bioactive Peptides and Peptide Derivatives of
;  TITLE OF INVENTION: Parathyroid Hormone (PTH) and Parathyroid
;  TITLE OF INVENTION: Hormone-Related Peptide (PTHrP)
;  FILE REFERENCE: 0609.4570001
;  CURRENT APPLICATION NUMBER: US/09/421,379
;  CURRENT FILING DATE: 1999-10-20
;  EARLIER APPLICATION NUMBER: U.S. 60/105,530
;  EARLIER FILING DATE: 1998-10-22
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: synthetic
;   OTHER INFORMATION: peptide
US-09-421-379-6

  Query Match             63.9%;  Score 39;  DB 4;  Length 9;
  Best Local Similarity   88.9%;  Pred. No. 3e+05;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 AVSEIQFMH 9
              |||||| ||
Db          1 AVSEIQLMH 9


RESULT 4
US-08-817-547A-2
; Sequence 2, Application US/08817547A
; Patent No. 6030790
;  GENERAL INFORMATION:
;    APPLICANT:  Adermann, Knut
;    APPLICANT:  Hock, Dieter
;    APPLICANT:  Magerlein, Markus
;    TITLE OF INVENTION:  Peptides from the hPTH Sequence
;    NUMBER OF SEQUENCES:  36
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Jones & Askew, LLP
;      STREET:  191 Peachtree Street, 37th Floor
;      CITY:  Atlanta
;      STATE:  Georgia
;      COUNTRY:  USA
;      ZIP:  30303
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/817,547A
;      FILING DATE:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/EP95/03757
;      FILING DATE:  29 SEPT 1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  FROST, ROGER T.
;      REGISTRATION NUMBER:  22,176
;      REFERENCE/DOCKET NUMBER:  07826-0007
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  404-818-3700
;      TELEFAX:  404-818-3799
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  9 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  unknown
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  peptide
;    HYPOTHETICAL:  no
;    ANTI-SENSE:  no
US-08-817-547A-2
```

```
  Query Match           59.0%;  Score 36;  DB 3;  Length 9;
  Best Local Similarity  77.8%;  Pred. No. 3e+05;
  Matches    7;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 AVSEIQFMH 9
              :|||| ||
Db          1 SVSEIQLMH 9


RESULT 5
US-09-421-379-7
; Sequence 7, Application US/09421379
; Patent No. 6495662
; GENERAL INFORMATION:
;  APPLICANT: Gardella, Thomas J.
;  APPLICANT: Kronenberg, Henry
;  APPLICANT: Potts, John T.
;  APPLICANT: Juppner, Harald
;  TITLE OF INVENTION: Bioactive Peptides and Peptide Derivatives of
;  TITLE OF INVENTION: Parathyroid Hormone (PTH) and Parathyroid
;  TITLE OF INVENTION: Hormone-Related Peptide (PTHrP)
;  FILE REFERENCE: 0609.4570001
;  CURRENT APPLICATION NUMBER: US/09/421,379
;  CURRENT FILING DATE: 1999-10-20
;  EARLIER APPLICATION NUMBER: U.S. 60/105,530
;  EARLIER FILING DATE: 1998-10-22
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: synthetic
;   OTHER INFORMATION: peptide
US-09-421-379-7

  Query Match           59.0%;  Score 36;  DB 4;  Length 9;
  Best Local Similarity  77.8%;  Pred. No. 3e+05;
  Matches    7;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 AVSEIQFMH 9
              |||||| :|
Db          1 AVSEIQLLH 9


RESULT 6
5460978-3
;Patent No. 5460978
;     APPLICANT: MARTIN, THOMAS J.;MOSELEY, JANE M.;KEMP,
;BRUCE E.;WETTENHALL, RICHARD E.H.
;     TITLE OF INVENTION: PROTEIN ACTIVE IN HUMORAL
;HYPERCALCEMIA OF MALIGNANCY-PTHRP
;     NUMBER OF SEQUENCES: 4
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/07/715,280
;       FILING DATE: 14-JUN-1991
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER: 199,235
;       FILING DATE: 09-MAY-1988
;       APPLICATION NUMBER:
;       FILING DATE:
;SEQ ID NO:3:
;       LENGTH: 11
5460978-3

  Query Match           50.8%;  Score 31;  DB 6;  Length 11;
  Best Local Similarity  70.0%;  Pred. No. 8.5;
  Matches    7;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 AVSEIQFMHN 10
              |||| |  ||
Db          1 AVSEHQLEHN 10


RESULT 7
US-09-421-379-8
; Sequence 8, Application US/09421379
; Patent No. 6495662
; GENERAL INFORMATION:
;  APPLICANT: Gardella, Thomas J.
;  APPLICANT: Kronenberg, Henry
;  APPLICANT: Potts, John T.
;  APPLICANT: Juppner, Harald
;  TITLE OF INVENTION: Bioactive Peptides and Peptide Derivatives of
;  TITLE OF INVENTION: Parathyroid Hormone (PTH) and Parathyroid
;  TITLE OF INVENTION: Hormone-Related Peptide (PTHrP)
;  FILE REFERENCE: 0609.4570001
;  CURRENT APPLICATION NUMBER: US/09/421,379
;  CURRENT FILING DATE: 1999-10-20
;  EARLIER APPLICATION NUMBER: U.S. 60/105,530
;  EARLIER FILING DATE: 1998-10-22
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: synthetic
;   OTHER INFORMATION: peptide
US-09-421-379-8

  Query Match           47.5%;  Score 29;  DB 4;  Length 9;
  Best Local Similarity  66.7%;  Pred. No. 3e+05;
  Matches    6;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 AVSEIQFMH 9
              |||| | :|
Db          1 AVSEHQLLH 9


RESULT 8
US-08-140-137A-42
; Sequence 42, Application US/08140137A
; Patent No. 5817617
;  GENERAL INFORMATION:
;    APPLICANT:  TUOMANEN, ELAINE
;    APPLICANT:  MASURE, H. R.
;    TITLE OF INVENTION:  ANALOGS OF ENDOTHELIAL LEUKOCYTE
;    TITLE OF INVENTION:  ADHESION MOLECULE (ELAM)
;    NUMBER OF SEQUENCES:  49
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Klauber & Jackson
;      STREET:  411 Hackensack Avenue
;      CITY:  Hackensack
;      STATE:  New Jersey
;      COUNTRY:  USA
;      ZIP:  07601
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/140,137A
;      FILING DATE:  27-MAY-1994
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Jackson Esq., David A.
;      REGISTRATION NUMBER:  26,742
;      REFERENCE/DOCKET NUMBER:  600-1-096
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  201 487-5800
;      TELEFAX:  201 343-1684
```

```
;      TELEX:  133521
;  INFORMATION FOR SEQ ID NO:  42:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  12 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;      DESCRIPTION:  CaRD peptide seqence
US-08-140-137A-42

  Query Match             47.5%;  Score 29;  DB 2;  Length 12;
  Best Local Similarity   62.5%;  Pred. No. 22;
  Matches    5;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 VSEIQFMH 9
              :|| ||:|
Db          5 ISEEQFVH 12


RESULT 9
US-08-817-547A-3
; Sequence 3, Application US/08817547A
; Patent No. 6030790
;  GENERAL INFORMATION:
;    APPLICANT:  Adermann, Knut
;    APPLICANT:  Hock, Dieter
;    APPLICANT:  Magerlein, Markus
;    TITLE OF INVENTION:  Peptides from the hPTH Sequence
;    NUMBER OF SEQUENCES:  36
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Jones & Askew, LLP
;      STREET:  191 Peachtree Street, 37th Floor
;      CITY:  Atlanta
;      STATE:  Georgia
;      COUNTRY:  USA
;      ZIP:  30303
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/817,547A
;      FILING DATE:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/EP95/03757
;      FILING DATE:  29 SEPT 1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  FROST, ROGER T.
;      REGISTRATION NUMBER:  22,176
;      REFERENCE/DOCKET NUMBER:  07826-0007
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  404-818-3700
;      TELEFAX:  404-818-3799
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  8 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  unknown
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  peptide
;    HYPOTHETICAL:  no
;    ANTI-SENSE:  no
US-08-817-547A-3

  Query Match             45.9%;  Score 28;  DB 3;  Length 8;
  Best Local Similarity   75.0%;  Pred. No. 3e+05;
  Matches    6;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 AVSEIQFM 8
              :||||| |
Db          1 SVSEIQLM 8


RESULT 10
US-08-482-228-42
; Sequence 42, Application US/08482228
; Patent No. 5968753
;  GENERAL INFORMATION:
;    APPLICANT:  Tseng-Law, Janet
;    APPLICANT:  Kobori, Joan A.
;    APPLICANT:  Al-Abdaly, Fahad A.
;    APPLICANT:  Guillermo, Roy
;    APPLICANT:  Helgerson, Sam L.
;    APPLICANT:  Deans, Robert J.
;    TITLE OF INVENTION:  POSITIVE AND POSITIVE/NEGATIVE CELL
;    TITLE OF INVENTION:  SELECTION MEDIATED BY PEPTIDE RELEASE
;    NUMBER OF SEQUENCES:  215
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Janice Guthrie, Ph.D.
;      STREET:  P.O. Box 15210
;      CITY:  Irvine
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  92713-5210
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/482,228
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Guthrie, Janice
;      REGISTRATION NUMBER:  35,170
;      REFERENCE/DOCKET NUMBER:  IT-4630CIP3
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (714) 440-5353
;      TELEFAX:  (714) 553-1952
;  INFORMATION FOR SEQ ID NO:  42:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  12 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-482-228-42

  Query Match             44.3%;  Score 27;  DB 2;  Length 12;
  Best Local Similarity   55.6%;  Pred. No. 54;
  Matches    5;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 AVSEIQFMH 9
              | | : |||
Db          3 ASSSVTFMH 11


RESULT 11
US-08-482-528-42
; Sequence 42, Application US/08482528
; Patent No. 6017719
;  GENERAL INFORMATION:
;    APPLICANT:  Tseng-Law, Janet
;    APPLICANT:  Kobori, Joan A.
;    APPLICANT:  Al-Abdaly, Fahad A.
;    APPLICANT:  Guillermo, Roy
;    APPLICANT:  Helgerson, Sam L.
;    APPLICANT:  Deans, Robert J.
;    TITLE OF INVENTION:  POSITIVE AND POSITIVE/NEGATIVE CELL
;    TITLE OF INVENTION:  SELECTION MEDIATED BY PEPTIDE RELEASE
;    NUMBER OF SEQUENCES:  215
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Janice Guthrie, Ph.D.
;      STREET:  P.O. Box 15210
;      CITY:  Irvine
```

```
;       STATE:  California
;       COUNTRY:  USA
;       ZIP:  92713-5210
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/482,528
;       FILING DATE:  07-JUN-1995
;       CLASSIFICATION:  435
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Guthrie, Janice
;       REGISTRATION NUMBER:  35,170
;       REFERENCE/DOCKET NUMBER:  IT-4630CIP4
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (714) 440-5353
;       TELEFAX:  (714) 553-1952
;   INFORMATION FOR SEQ ID NO:  42:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  12 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  peptide
US-08-482-528-42

  Query Match             44.3%;  Score 27;  DB 3;  Length 12;
  Best Local Similarity   55.6%;  Pred. No. 54;
  Matches    5;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 AVSEIQFMH 9
              | | : |||
Db          3 ASSSVTFMH 11


RESULT 12
US-09-421-379-10
; Sequence 10, Application US/09421379
; Patent No. 6495662
; GENERAL INFORMATION:
;  APPLICANT: Gardella, Thomas J.
;  APPLICANT: Kronenberg, Henry
;  APPLICANT: Potts, John T.
;  APPLICANT: Juppner, Harald
;  TITLE OF INVENTION: Bioactive Peptides and Peptide Derivatives of
;  TITLE OF INVENTION: Parathyroid Hormone (PTH) and Parathyroid
;  TITLE OF INVENTION: Hormone-Related Peptide (PTHrP)
;  FILE REFERENCE: 0609.4570001
;  CURRENT APPLICATION NUMBER: US/09/421,379
;  CURRENT FILING DATE: 1999-10-20
;  EARLIER APPLICATION NUMBER: U.S. 60/105,530
;  EARLIER FILING DATE: 1998-10-22
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
;   LENGTH: 9
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: synthetic
;   OTHER INFORMATION: peptide
US-09-421-379-10

  Query Match             42.6%;  Score 26;  DB 4;  Length 9;
  Best Local Similarity   55.6%;  Pred. No. 3e+05;
  Matches    5;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 AVSEIQFMH 9
              :||| | :|
Db          1 SVSEHQLLH 9


RESULT 13
US-08-116-778E-9
; Sequence 9, Application US/08116778E
; Patent No. 5830470
; GENERAL INFORMATION:
;   APPLICANT:  NAKAMURA, KAZUYASU
;   APPLICANT:  KOIKE, MASAMICHI
;   APPLICANT:  SHITARA, KENYA
;   APPLICANT:  HANAI, NOBUO
;   APPLICANT:  KUWANA, YOSHIHISA
;   APPLICANT:  HASEGAWA, MAMORU
;   TITLE OF INVENTION:  HUMANIZED ANTIBODIES
;   NUMBER OF SEQUENCES:  49
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE:  NIXON & VANDERHYE P.C.
;     STREET:  1100 NORTH GLEBE ROAD
;     CITY:  ARLINGTON
;     STATE:  VIRGINIA
;     COUNTRY:  U.S.A.
;     ZIP:  22201-4714
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE:  Floppy disk
;     COMPUTER:  IBM PC compatible
;     OPERATING SYSTEM:  PC-DOS/MS-DOS
;     SOFTWARE:  PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER:  US/08/116,778E
;     FILING DATE:  07-SEP-93
;     CLASSIFICATION:  424
;   ATTORNEY/AGENT INFORMATION:
;     NAME:  WILSON, MARY J.
;     REGISTRATION NUMBER:  32,955
;     REFERENCE/DOCKET NUMBER:  249-59
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE:  (703)816-4000
;     TELEFAX:  (703)816-4100
;  INFORMATION FOR SEQ ID NO:  9:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH:  10 amino acids
;     TYPE:  amino acid
;     TOPOLOGY:  linear
;   MOLECULE TYPE:  peptide
US-08-116-778E-9

  Query Match             41.0%;  Score 25;  DB 2;  Length 10;
  Best Local Similarity   44.4%;  Pred. No. 1.1e+02;
  Matches    4;  Conservative    2;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 AVSEIQFMH 9
              | | : :||
Db          2 ASSSVSYMH 10


RESULT 14
US-08-438-562-9
; Sequence 9, Application US/08438562
; Patent No. 5874255
; GENERAL INFORMATION:
;   APPLICANT:  NAKAMURA, KAZUYASU
;   APPLICANT:  KOIKE, MASAMICHI
;   APPLICANT:  SHITARA, KENYA
;   APPLICANT:  HANAI, NOBUO
;   APPLICANT:  KUWANA, YOSHIHISA
;   APPLICANT:  HASEGAWA, MAMORU
;   TITLE OF INVENTION:  HUMANIZED ANTIBODIES
;   NUMBER OF SEQUENCES:  49
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE:  NIXON & VANDERHYE P.C.
;     STREET:  1100 NORTH GLEBE ROAD
;     CITY:  ARLINGTON
;     STATE:  VIRGINIA
;     COUNTRY:  U.S.A.
;     ZIP:  22201-4714
```

```
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/438,562
;      FILING DATE:  10-MAY-95
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/116,778
;      FILING DATE:  07-SEP-93
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  WILSON, MARY J.
;      REGISTRATION NUMBER:  32,955
;      REFERENCE/DOCKET NUMBER:  249-76
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (703)816-4000
;      TELEFAX:  (703)816-4100
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-438-562-9

  Query Match             41.0%;  Score 25;  DB 2;  Length 10;
  Best Local Similarity   44.4%;  Pred. No. 1.1e+02;
  Matches    4;  Conservative    2;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 AVSEIQFMH 9
              | |  : :||
Db          2 ASSSVSYMH 10


RESULT 15
US-08-483-528B-97
; Sequence 97, Application US/08483528B
; Patent No. 5939532
;  GENERAL INFORMATION:
;    APPLICANT:  NAKAMURA, KAZUYASU
;    APPLICANT:  KOIKE, MASAMICHI
;    APPLICANT:  SHITARA, KENYA
;    APPLICANT:  HANAI, NOBUO
;    APPLICANT:  KUWANA, YOSHIHISA
;    APPLICANT:  HASEGAWA, MAMORU
;    TITLE OF INVENTION:  HUMANIZED ANTIBODIES
;    NUMBER OF SEQUENCES:  103
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  NIXON & VANDERHYE P.C.
;      STREET:  1100 NORTH GLEBE ROAD
;      CITY:  ARLINGTON
;      STATE:  VIRGINIA
;      COUNTRY:  U.S.A.
;      ZIP:  22201-4714
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/483,528B
;      FILING DATE:  07-JUN-95
;      CLASSIFICATION:  536
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (703)816-4000
;      TELEFAX:  (703)816-4100
;  INFORMATION FOR SEQ ID NO:  97:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  10 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-483-528B-97

  Query Match             41.0%;  Score 25;  DB 2;  Length 10;
  Best Local Similarity   44.4%;  Pred. No. 1.1e+02;
  Matches    4;  Conservative    2;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 AVSEIQFMH 9
              | |  : :||
Db          2 ASSSVSYMH 10


Search completed: September  5, 2004, 09:38:33
Job time : 11 secs
```